



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 1653

TO: Rosanne Kosson
Art Unit: 1653
Location: REM-3B84&3C18
Serial Number: 09/856723

Tuesday, May 23, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>. If the result files have been separated into two (2) or more versions, you may view additional files via the select "View version list for this application" link.

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).



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190532

From: Kosson, Rosanne
 Sent: Thursday, May 18, 2006 3:55 PM
 To: STIC-Biotech/ChemLib
 Subject: request for sequence search- 09/856,723- REGULATORY PROTEIN PKE#83 FROM HUMAN KERATINOCTYES

Please search SEQ ID NO: 8 for me in the commercial and interference databases. This is a protein of 1076 amino acids.
 My mailbox is in 3C70. Thanks!!!

Rosanne Kosson
 Patent Examiner, AU 1653
 REM 3B84
 571-272-2923
 rosanne.kosson@uspto.gov

aa 1076

P03 N119199 PCA

12/7/98 DE ? no

11/26/98 DE ? no

PCA/DE 90/03732

S03/2007
URFESEARCHED
INDEXED
SERIALIZED
FILED
MAY 18 2006
USPTO-CHICAGO
RECEIVED
MAY 22 2006
USPTO-CHICAGO5/22
AT

ME

 Searcher: _____
 Searcher Phone: _____
 Date Searcher Picked up: _____
 Date completed: _____
 Searcher Prep Time: _____
 Online Time: _____

 Type of Search
 NA# _____ AA# _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

 Vendors and cost where applicable
 STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other (Specify): _____

Date completed: _____
 Searcher: Beverly e 2528
 Terminal time: _____
 Elapsed time: _____
 CPU time: _____
 Total time: _____
 Number of Searches: _____
 Number of Databases: _____

Search Site

____ STIC
 ____ CM-1
 ____ Pre-S

Type of Search

____ N.A. Sequence
 ____ A.A. Sequence
 ____ Structure
 ____ Bibliographic

Vendors

____ IG
 ____ STN
 ____ Dialog
 ____ APS
 ____ Geninfo
 ____ SDC
 ____ DARC/Questel
 Other CGN

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

May 20, 2006, 17:05:42 ; Search time 320 Seconds

(without alignments)
3110.365 Million cell updates/secTitle:
Perfect score:

US-09-856-723a-8

Sequence:

1 MKQYASFMPQTQTDVKLKFKP RTLEQNKGKOMAKKEBKKVQLQ 1076

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched:

2849598 seqs, 925115592 residues

Total number of hits satisfying chosen parameters:

2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2;*

2: uniprot_sprot;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1196	2 Q6QNV2_HUMAN
2	5442.5	99.2	1231	2 Q8NDL1_HUMAN
3	5266	95.9	1160	2 Q6NXY2_HUMAN
4	4919	89.6	962	2 Q9X7T7_HUMAN
5	4683.5	85.3	1242	2 Q69ZM3_MOUSE
6	4522	82.9	1206	2 Q5OK32_MOUSE
7	4522	82.6	1205	2 Q9ZQ66_MOUSE
8	4414.5	80.4	893	2 Q53TV6_HUMAN
9	4226.5	41.3	1036	2 Q4SGB9_TEETING
10	1154.5	21.0	762	2 Q5QH32_RAT
11	1151.5	21.0	874	2 Q1J977_MOUSE
12	1131	20.6	759	2 Q9MS6_MOUSE
13	1127	20.5	771	2 Q9PM55_MOUSE
14	1082	19.7	723	2 Q8C2W6_MOUSE
15	1076.5	19.6	987	2 Q9V7X1_DRONC
16	1075.5	19.6	987	2 Q8MR33_DRONC
17	1018.5	18.6	987	2 Q7PKB6_ANOCA
18	966	17.6	310	2 Q9NW19_HUMAN
19	~950.5	17.3	1716	2 Q9MS77_MOUSE
20	945.5	17.2	1415	2 Q9H7W7_HUMAN
21	941.5	17.2	1510	2 Q8N3D4_HUMAN
22	895	16.3	308	2 Q5QK22_MOUSE
23	850.5	15.5	1919	2 Q4RIP0_TEETING
24	627	11.4	125	2 Q53TG7_HUMAN
25	579.5	10.6	288	2 Q4SGC0_TEETING
26	556	10.1	243	2 Q8TB88_HUMAN
27	507.5	9.2	1010	2 Q9VN34_DRONC
28	498.5	9.1	863	1 MILKL1_HUMAN
29	480.5	8.8	967	2 Q6GNGU2_XENIA
30	480	8.7	870	1 MILKL6_MOUSE
31	467.5	8.5	1886	2 Q4T7H5_TEETING

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2: uniprot_trembl;*

Searched:

2849598 seqs, 925115592 residues

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2849598

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

RG	The German CDNA Consortium;
RA	Ottenwaelde B., Obermaier B., Deutschenbaur S., Schlaipper A., Wiemann S.;
RA	Mewes H.W., Weil C., Auld C., Osanger A., Bobo G., Han M., Wiemann S.;
RL	Submitted ('SEP-2004') to the EMBL/GenBank/DDBJ databases.
RN	[12]
RP	NUCLEOTIDE SEQUENCE.
RA	Castellano-Munoz M., Fernandez-Chacon R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RL	CC
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NonDeriva License
DR	EMBL; ALB3958; CAD38814.1; -; mRNA.
DR	EMBL; AV331186; AJQ97141.1; -; mRNA.
DR	HSSP; Q0182; 1BKR.
DR	Ensembl; BNG300000115504; Homo sapiens.
DR	HGNC; HGNC:23144; EBP1.
DR	InterPro; IPR001715; Calponin_act_bd.
DR	Pfam; PF00307; CH; 1.
DR	SMART; SNO013; CH; 1.
DR	PROSITE; PS50021; CH; 1.
KW	Hypothetical protein.
SEQUENCE	1231 AA; 139858 MW; DB7A7DBE572AEB9B CRC64;
Query Match	99.2%; Score 542.5; DB 2; Length 1231;
Best Local Similarity	96.6%; Pred. No. 4.1e-205;
Matches	1073; Conservative 1; Mismatches 2; Indels 35; Gaps 1;
Qy	1 MKQYASPMPTQTDYKKEPKLKVVAALQFSLSCIFIREGRATDPMOSLASLVSQK
Db	121 MKQYASPMPTQTDYKKEPKLKVVAALQFSLSCIFIREGRATDPMOSLASLVSQK
Qy	61 ADICNLDPEDDNEPDENRVRNGEKAAKIT-----91
Db	181 ADICNLDPEDDNEPDENRVRNGEKAAKITGIVNOLNALSLSLBDODC1KQANMRSAK
Qy	92 -----ELINKAFLDEAKDLATVNSMPDDDAELNPFGJPDSEPIETASPRKE 145
Db	241 SASSEEELINKAFLDEAKDLATVNSMPDDDAELNPFGJPDSEPIETASPRKE 300
Qy	146 DSPTNSTNPPEKSYTPTQYLPFDEPAFTKIDSPPOSTKRNIRPYDMSLYADSK 205
Db	421 AGKDLSTSPKPSIPIPSPVIGRKENASOSILWVCKEVTKNYGVKINTFTSWRGLSICA 325
Qy	326 ILMHFRPLDIDYKSLNPDKIENKKAYDGASIGISLPLESDMVLIAIPDKLTWMTL 385
Db	481 ILMHFRPLDIDYKSLNPDKIENKKAYDGASIGISLPLESDMVLIAIPDKLTWMTL 540
Qy	206 TEEERLDOSNPTEPKSTPPPNLVPQELTERVVKAPAPPVLSPTKVLNENTV 265
Db	361 TEERELDSESNPFTEPKSTPPPNLVPQELTERVVKAPAPPVLSPTKVLNENTV 420
Qy	265 AGKDLSTSPKPSIPIPSPVIGRKENASOSILWVCKEVTKNYGVKINTFTSWRGLSICA 325
Db	421 AGKDLSTSPKPSIPIPSPVIGRKENASOSILWVCKEVTKNYGVKINTFTSWRGLSICA 480
Qy	326 ILMHFRPLDIDYKSLNPDKIENKKAYDGASIGISLPLESDMVLIAIPDKLTWMTL 385
Db	481 ILMHFRPLDIDYKSLNPDKIENKKAYDGASIGISLPLESDMVLIAIPDKLTWMTL 540
Qy	386 YQRAHSGQELNVQLEENNSKSTKYGVNEYDTNSVQDKFYAEISDLKREPELQQP 445
Db	541 YQRAHSGQELNVQLEENNSKSTKYGVNEYDTNSVQDKFYAEISDLKREPELQQP 600
Qy	446 ISGAVDFLSQDQISVFVNDSGVVERSESESHOTPDDHSSTASPVCRTKSDTEPKOQSOSS 505
Db	601 ISSAVDFLSQDQISVFVNDSGVVERSESESHOTPDDHSSTASPVCRTKSDTEPKOQSOSS 660
Qy	506 GRVTS3SDPGISNTSDQAOQLGKRLKATKELSDLYSDKKDMSPPICTEDE 565
Db	661 GRVTS3SDPGISNTSDQAOQLGKRLKATKELSDLYSDKKDMSPPICTEDE 720
Qy	566 QKLQTLDIGSNREKEKLENSRLECRSDPESIPIKTSLSPTSPKLGYSYSDLAKKHA 625
Db	721 QKLQTLDIGSNREKEKLENSRLECRSDPESIPIKTSLSPTSPKLGYSYSDLAKKHA 780
RN	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Kidney;

Db 781 SLRQTESDPDADRTTINHADHSKIVOHRLISRQEELKERVILLEQARRDAALKAGNKH 840
 RA Director MGC Project; to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC
 Qy 686 NTNTATPPCNCNQLSQQDERRQERAROLAEARSQGUMSEPSYGEMAEKLERS 745
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 Db 841 NTNTATPPCNCNQLSQQDERRQERAROLAEARSQGUMSEPSYGEMAEKLERS 900
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 DR EMBL; BC067215; AAH67215.1; - ; mRNA.
 DR HSSP; Q01082; IAA2.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR Pfam; PF00307; CH; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS50021; CH; 1.
 SQ SEQUENCE 1160 AA; 13232 MW; DD7923PE0B14AF11 CRC64;
 Query Match 95.9%; Score 566; DB 2; Length 1160;
 Best Local Similarity 96.6%; Pred. No. 3.2e-198;
 Matches 1039; Conservative 1; Mismatches 0; Indels 36; Gaps 1;
 Qy 926 LENEOKQIDTRALVERKLRYLMDTGRNTBEAMQEWMLVNCKNALTRMQLSL 985
 Db 1081 LENEOKQIDTRALVERKLRYLMDTGRNTBEAMQEWMLVNCKNALTRMQLSL 1140
 Qy 986 KEDHDLERRYILNLNRILRAMIAIEDAQTKRQKRQFQLLDEFLVALVNKDADLDAOR 1045
 Db 1141 KEDHDLERRYILNLNRILRAMIAIEDAQTKRQKRQFQLLDEFLVALVNKDADLDAOR 1200
 Qy 1046 KQAFEDDEHLERTLEONKGIAKKEBKCVLQ 1076
 Db 1201 KQAFEDDEHLERTLEONKGIAKKEBKCVLQ 1231
 RESULT 3
 Q6NK72_HUMAN PRELIMINARY; PRT; 1160 AA.
 AC Q6NK72; 05-JUL-2004, integrated into UniProtKB/TREMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DR EHBL1 protein.
 GN Name=EHBL1;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo sapiens (Human);
 OC Homo;
 NCBI_TAXID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Uterus;
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Degeorge J., Wagner L., Shevchenko C.M., Schuler G.D.,
 RA Klaunier R.D., Collins P.S., Wagner L., Shevchenko C.M., Schuler G.D., Bhat N.K.,
 RA Atschul S.F., Zieberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Haehn F.,
 RA Diatchenko L., Matsushita K., Farmer A.A., Robin G.M., Hong J.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udini T.B., Toshiyuki I., Carninci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peers G.J., Abramson R.D., Mulahay S.J.,
 RA Boseck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsette P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Gibbs J.,
 RA Fahey J., Heaton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko P., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butler Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnurch A., Schein J.B., Jones S.J.M., Marra M.A.; Smallius D.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 DR EMBL; BC067215; AAH67215.1; - ; mRNA.
 DR HSSP; Q01082; IAA2.
 DR InterPro; IPR001715; Calponin_act_bd.
 DR Pfam; PF00307; CH; 1.
 DR SMART; SM00033; CH; 1.
 DR PROSITE; PS50021; CH; 1.
 SQ SEQUENCE 1160 AA; 13232 MW; DD7923PE0B14AF11 CRC64;
 Query Match 95.9%; Score 566; DB 2; Length 1160;
 Best Local Similarity 96.6%; Pred. No. 3.2e-198;
 Matches 1039; Conservative 1; Mismatches 0; Indels 36; Gaps 1;
 Qy 1 MKQYASPMPTQTDYKLKEPLSKVVAQSQSICFREGKATDBMQSLASLMSMKQ 60
 Db 121 MKQYASPMPTQTDYKLKEPLSKVVAQSQSICFREGKATDBMQSLASLMSMKQ 180
 Qy 61 ADIGNLDFFEDNEDDENRNUOZEKAAKITELINKLNFLDEAKDQDATNSNPFDPPA 120
 Db 181 ADIGNLDFFEDNEDDENRNUOZEKAAKITELINKLNFLDEAKDQDATNSNPFDPPA 240
 Qy 121 AELUPFGDDSEEPETETASPRKTEDSFNSTSNPKEVQTPQYLPDPDEPEARTKDS 180
 Db 241 AELUPFGDDSEEPETETASPRKTEDSFNSTSNPKEVQTPQYLPDPDEPEARTKDS 300
 Qy 181 PPQSTKRKTRPVDMSKVLYADSSKTRERELDSENPPFPKSTPPPNVLNPQBLETER 240
 Db 301 PPQSTKRKTRPVDMSKVLYADSSKTRERELDSENPPFPKSTPPPNVLNPQBLETER 360
 Qy 241 RVKRKAPAPVPLSRTKGVMENTVSAGKDLSTSPPKSPSIPSPVPLGKRNKNAQSLSLWCKE 300
 Db 361 RVKRKAPAPVPLSRTKGVMENTVSAGKDLSTSPPKSPSIPSPVPLGKRNKNAQSLSLWCKE 420
 Qy 301 VTKVYRGVKLTINFSTSWNGLSCAILHRFPDLIDVSINPDKKENKKAVGFAIG 360
 Db 421 VTKVYRGVKLTINFSTSWNGLSCAILHRFPDLIDVSINPDKKENKKAVGFAIG 480
 Qy 361 ISRLIEPSDMVLLAIPDGKLTWMTLYQRAHFSQELINVOISENSSISTKYGNDT 420
 Db 481 ISRLIEPSDMVLLAIPDGKLTWMTLYQRAHFSQELINVOISENSSISTKYGNDT 540
 Qy 421 NSSYDQEKFYAEISDLKRPBPELLOOPISGAVDPLSDODDSVPNDSGVGSESEHQTPDPL 480
 Db 541 NSSYDQEKFYAEISDLKRPBPELLOOPISGAVDPLSDODDSVPNDSGVGSESEHQTPDPL 600
 Qy 481 SPSPASPPCRTESDTEPKQSQSSGRGSGDPGICNTDSTAQVILGKELKASTL 540
 Db 601 SPSPASPPCRTESDTEPKQSQSSGRGSGDPGICNTDSTAQVILGKELKASTL 660
 Qy 541 BLSLIVSYDKKOMSPPFCEEDBQKQTDLGSNLAKKEKLNSRSBCRSBESPDK 600
 Db 661 ELSLIVSYDKKOMSPPFCEEDBQKQTDLGSNLAKKEKLNSRSBCRSBESPDK 720
 Qy 601 TSLSPTSKLGYYSRSDLIAKKHHSILOTESDADRTLNHADHSKIVORHLLSQE 660
 Db 721 TSLSPTSKLGYYSRSDLIAKKHHSILOTESDADRTLNHADHSKIVORHLLSQE 780
 Qy 661 ELKERRAVILLEQARRDAALKAGNKTNTATPCNROSDQDQDERRQERAROLAE 720
 Db 781 ELKERRAVILLEQARRDAALKAGNKTNTATPCNROSDQDQDERRQERAROLAE 840
 Qy 721 ARSGVKKMRLPSYGEMAEKLERSKGENDNIEIDTNBEPGFVGGGDLTNIEN 780
 Db 841 ARSGVKKMRLPSYGEMAEKLERSKG----- 869
 Qy 781 DLDTPEQNSKLVDLKJKLLEVOPQVANSPPSSAQAVTTESSQDMKGSTEDIRTERIQLQ 840
 Db 870 -----EQNSKLVDLKJKLLEVOPQVANSPPSSAQAVTTESSQDMKGSTEDIRTERIQLQ 924

QY 841 TTERFRNPVVFSDKSTVRKTOLQSPSQYIENRPEMKORSIQEDTKKGNEBEKAITEQR 900
Db 925 TTERFRNPVVFSDKSTVRKTOLQSPSQYIENRPEMKORSIQEDTKKGNEBEKAITEQR 984
Qy 901 KPRDEDEVALKGFKDTSQYVQGYELAKALENEQKIDTRALVEKLURYLMDTGRTEERAM 950
Db 985 KPSBDEVALKGFKDTSQYVQGYELAKALENEQKIDTRALVEKLURYLMDTGRTEERAM 950
Qy 961 MQEWPMLVNKGALIRRMNQLSLRKEDLERRYELNLREBLRMLAIEDWQKTAQKRE 1020
Db 1045 MQEWPMLVNKGALIRRMNQLSLRKEDLERRYELNLREBLRMLAIEDWQKTAQKRE 1104
Qy 1021 QLLIDDELVALVNLNKDALVRDLDQEQKQABEEDEHLERTLEQKGMACKEKCVLQ 1076
Db 1105 QLLIDDELVALVNLNKDALVRDLDQEQKQABEEDEHLERTLEQKGMACKEKCVLQ 1160

RESULT 4

094977 HUMAN PRELIMINARY; PRT; 962 AA.
ID 094977_HUMAN
AC 094977
DT 01-MAY-1999, integrated into UniProtKB/TREMBL.
DT 07-FEB-2006, entry version 24.
DE KIAA0903 protein (Fragment).
GN Name=KIAA0903;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Buthera; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TAXID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RD MEDLINE=99156230; PubMed=10048485; DOI=10.1093/dnareg/5.6.355;
RX RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroswa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.;"
RL Refs. 5:355-364(1998).

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DR EMBL; AB020710; BAA74926.1; -; mRNA.
DR RSP; Q01082; IBCR.
DR Ensembl; ENSG00000115504; Homo sapiens.
DR InterPro; IPR001715; Calponin_act_bdb.
DR SMART; SM00033; CH; 1.
DR PROSITE; PS50021; CH; 1.
DR PT NOD TER 1
SQ SEQUENCE 962 AA; 109413 MW; 58BBC315D322D7AB CRC64;

Query Match 89.6%; Score 4919; DB 2; Length 962;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 FDDPDAESELNPFGDPDSRPTTASPRKTEFSPYNNSYNPKEVQTPQYIAPRDFEAF 174
Db 1 FDDPDAESELNPFGDPDSRPTTASPRKTEFSPYNNSYNPKEVQTPQYIAPRDFEAF 60
Qy 175 VTKDSDPPOSTKRNIRUDMCKLYADSSKTEERELDESNPYPTEPKSTPPNLYVPO 234
Db 61 VTKDSDPPOSTKRNIRUDMCKLYADSSKTEERELDESNPYPTEPKSTPPNLYVPO 120
Qy 235 ELETERRYRKKAAPPVSPKTYGVLENNTVSAGKDLSTSPKUSPISPVSLGRKPNASQL 294
Db 121 ELETERRYRKKAAPPVSPKTYGVLENNTVSAGKDLSTSPKUSPISPVSLGRKPNASQL 180
Qy 295 IWKCKEVTKNRYRQVKITNFTTSWNGLSFCATLHFRPDPLIVYKSLNPQDIEKKAYD 354

Db 181 LWVCGEVTKNRYRQVKITNFTTSWNGLSFCATLHFRPDPLIVYKSLNPQDIEKKAYD 240
Qy 355 GFSASIGSRLPSLSDMILALIDKLTWTYQIYRAHSQBLNVOIERNISKSTYVG 414
Db 241 GFSASIGSRLPSLSDMILALIDKLTWTYQIYRAHSQBLNVOIERNISKSTYVG 300
Qy 415 NYETDTNSVDOBKFYALSLKREPLOQPSQAVFLQSPQDODSVFNDGVSGESEHQ 474
Db 301 NYETDTNSVDOBKFYALSLKREPLOQPSQAVFLQSPQDODSVFNDGVSGESEHQ 360
Qy 475 TPDHLSRSTASPYCRRKTSDFBPKQSQQSGRTGSDPGCSNTSTQAVTLGKRL 534
Db 361 TPDHLSRSTASPYCRRKTSDFBPKQSQQSGRTGSDPGCSNTSTQAVTLGKRL 420
Qy 535 LKARTLESLYVSKDKDMSPPICETDEBKQLQTLIGSNLEKEKLENSLCECRSDP 594
Db 421 LKARTLESLYVSKDKDMSPPICETDEBKQLQTLIGSNLEKEKLENSLCECRSDP 480
Qy 595 ESPICKTSLSPTSKLGYSYSRDLAKKHSRQTESPDADRTLNHADSSKIVQHR 654
Db 481 ESIKKTSLSPTSKLGYSYSRDLAKKHSRQTESPDADRTLNHADSSKIVQHR 540
Qy 655 LASRQEBSKERARVLLQGARRDAALKAGKNGINTNTAPFCNRQLSDQODEERRRLERA 714
Db 541 LLSRQEBSKERARVLLQGARRDAALKAGKNGINTNTAPFCNRQLSDQODEERRRLERA 600
Qy 715 ROLIARARSGVQMSLPSYGENAAEKERSKAGBENDNEFIDTNEEIPGFVWGGDE 774
Db 601 ROLIARARSGVQMSLPSYGENAAEKERSKAGBENDNEFIDTNEEIPGFVWGGDE 660
Qy 775 LTMLENDLDTPRONSKWDLKUKKLLVQPOVANSSSAAQAVTSESQDMKSGTEDLR 834
Db 661 LTMLENDLDTPRONSKWDLKUKKLLVQPOVANSSSAAQAVTSESQDMKSGTEDLR 720
Qy 835 TERLQKTERFRNPVVFSDKSTVRKTOLQSPSQYIENRPEMKORSIQEDTKKGNEBEKA 894
Db 721 TERLQKTERFRNPVVFSDKSTVRKTOLQSPSQYIENRPEMKORSIQEDTKKGNEBEKA 780
Qy 895 ITETQRKPSEDEVALKGFKDTSQYVQGYELAKALENEQKIDTRALVEKLURYLMDTGRNT 954
Db 781 ITETQRKPSEDEVALKGFKDTSQYVQGYELAKALENEQKIDTRALVEKLURYLMDTGRNT 840
Qy 955 ESEBAMQEWMLVNKGALIRRMNQLSLRKEDLERRYELNLREBLRMLAIEDQKTE 1014
Db 841 ESEBAMQEWMLVNKGALIRRMNQLSLRKEDLERRYELNLREBLRMLAIEDQKTE 900
Qy 1015 ADKRBQBLDLSLVALVNLNKDALVRDLDQEQKABEEDEHLERTLEQKGMACKEKCV 1074
Db 901 ADKRBQBLDLSLVALVNLNKDALVRDLDQEQKABEEDEHLERTLEQKGMACKEKCV 960
Qy 1075 LQ 1075
Db 961 LQ 962

RESULT 5

069ZM3 MOUSE PRELIMINARY; PRT; 1242 AA.
ID 069ZM3_MOUSE
AC 069ZM3
DT 13-SEP-2004, integrated into UniProtKB/TREMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DB MKIAA0903 protein (fragment).
GN Name=Bhbp1; Synonyms=mkiaa0903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Buthera; Euarchontoglires; Gires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mous.
OX NCBI_TAXID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;

RX Pubmed=15368895; DOI=10.1093/dnarecs/11.3.205;
 RA Okamoto N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S.,
 RA Saga Y., Seino S., Nishimura M., Kaihori T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.;
 RT Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT IV. The complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.;
 RL DNA Res. 11:205-218(2004).

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DR EMBL; AKU73055; BAD32333.1; -; mRNA.

DR Ensembl; ENSMUSG00000042302; Mus musculus.

DR MGI; MGI-2667252; Ebhp1; Muus musculub.

DR GO; GO:0005515; F_protein_binding; IPI.

DR InterPro; IPR01715; Calponin_act_bd.

DR Pfam; PF00307; CH; 1.

DR SMART; SM0033; CH; 1.

DR PROSITE; PS50021; CH; 1.

FT NON_TER 1

SQ SEQUENCE 1242 AA; 140356 MW; 1C8D17FC63BC0932 CRC64;

Query Match 85.3%; Score 4633.5; DB 2; Length 1242;
 Best Local Similarity 84.1%; Pred. No. 2.2e-175;
 Matches 945; Conservative 40; Mismatches 78; Indels 61; Gaps 10;

QY 1 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSLSCLIFREGKATDEDMOSLASLVSMQ 60

Db 132 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSLSCLIFREGKATDEDMOSLASLVSMQ 60

QY 61 ADIGNLDDFEDNEDDENRNQEEAKLT----- 91

Db 192 ADIGNLDDFEDNEDDENRNQEEAKLT----- 251

QY 92 -----BLINKLNFLDAEKDLATNSNPFDPPDAARIANPFGDDSERPITETASPRKE 145

Db 252 SASSEBSELINTNLFEDEAKDLATNTNPFDPPDTAEPEAFVTKOSPPQSTRKRNTRPVMSKLYADSK 311

QY 146 DSFYNNSYNPKFKEVQTPQYIAMPDFDEPEAFVTKOSPPQSTRKRNTRPVMSKLYADSK 205

Db 312 BSFTNNSCPFFKGIVQTPOIAMPFDPEPETFMKIKSPPSQSTRRKLRPVMSKLYADSK 371

QY 206 TEERLDENSNPPYEPKPT-SPPNLVNTVQEGETERRVRKRAPAPPAPLAPPAPPALT 253

Db 372 S-EBBELDESNPPYEPKPT-SPPNLVNTVQEGETERRVRKRAPAPPAPLAPPAPPALT 429

QY 254 PKTGVLNET-VSAGKDLSPTSPKSPISPVPLGRKPNASOSSLWCKEVTNKTRGVKTN 312

Db 430 PKTGVL-NENTVWSAGKDLSPTSPKSPISPVPLGRKPNASOSSLWCKEVTNKTRGVKTN 488

QY 313 FTTSWRNGLSSFCATAAHFRFDLIDYKSLNPODIKENKKAYDGASTIGSRLEPSDMV 372

Db 489 FTTSWRNGLSSFCATAAHFRFDLIDYKSLNPODIKENKKAYDGASTIGSRLEPSDMV 548

QY 373 LAIPDKLTVWYLQIRAMPSQELNVWENNSKSTKVGYNEPDTSVDPDKFVAR 432

Db 549 LAIPDKLTVWYLQIRAMPSQELNVWENNSKSTKVGYNEPDTSVDPDKFVAR 608

QY 433 LSDLKRKEPLQQPSGAVIDLSQDSVFPNDGSVQBSSESHQTDDHSPSTASPYCRT 492

Db 609 LSDLKRKEPLQQPSGAVIDLSQDSVFPNDGSVQBSSESHQTDDHSPSTASPYCRT 668

QY 493 KSDTRPQKSQSGSGRTGSGDPPGICSNNTSTQAQVTLGKERRLLKARTELSLDLYVSDKCK 552

Db 669 KSDTRPQKSQSGSGRTGSGDPPGICSNNTSTQAQVTLGKERRLLKARTELSLDLYVSDKCK 727

QY 553 DMSPPFICBETBDOKLQTLIGSNUKEKLENNLSLECRSPERSPIKYLSPSKLAYS 612

Db 728 DVSP---LSAYEQOKLQTVHASSDMEQKMKRSLSLCRUDGELAITKPNVSSPSKLG-- 781

613 YSRDLDLAKKKHASLRQTESDPADRTTINHADHSKIVQHRLLSRQEBSLKERARVLUHQ 672

Db 782 YNRDIDFTKPCASLQRQSRSDDPAKNTLHADHNPKAVOHMLRSQEELKERARVLUHQ 841

QY 673 ARDDALKAGKHNWINTATPPCNQNLSDQDDEERRQRARRQLIAEARSGVMSLPS 732

Db 842 ARDDAKYKGSKHGSAAALCSIQNDQESRRQRARRQLIAEARSGVMSLPS 901

QY 733 YGEMARAKJUKERSKASGDENDNIEIDTNBRIPEGFVGGDELNLENDLDTPEONSKLV 792

Db 902 YGEMARAKJUKERSKASGDENDNIEIDTNBRIPEGFVGGDELNLENDLDTPEONSKLV 961

QY 793 DLKUKGLLSTTOPQVANSREASAOKVTSSEBODUKSGTSDRTERLQTYTERFNPVVIS 852

Db 962 DLRLKRLQEAQPOVANLPLSAOAKVTRASEQGERSGVQDVLTERLQATERFRNPVVIS 1021

QY 853 KDSTVRKTOLOSFQYIENRPEMGRORSQEDTICKGNENKAATETQRKPSDEVLNKG 912

Db 1079 KDTSTVRKTOLOSFQYIENRPEMGRORSQEDTICKGNENKAATETQRKPSDEVLNKG 1138

Db 1022 KDTSTVRKTOLOSFQYIENRPEMGRORSQEDTICKGNENKAATETQRKPSDEVLNKG 1078

QY 913 KDTQSYVVBRAALENEQOIDTRAILVTRKLRYIMDCTGNTZEEAMMQEWFLVNKG 972

Db 1139 ALIRRMNQISLLEKEHDERRVYELNRELRLRAMLAEDWORTEAQERREQOLLLDBLVALVD 1198

QY 1033 KRDALVRLDQAQEKAERDEHLRLTIEQNGKMAKKEKCVLQ 1076

Db 1199 KRDALVRLDQAQEKAERDEHLRLTIEQNGKMAKKEKCVLQ 1242

RESULT 6

QSOX3_MOUSE

ID QSOX3_MOUSE PRELIMINARY; PRT; 1206 AA.

AC QSOX3;

DT 21-DEC-2004, integrated into UniProtKB/TREMBL.

DT 21-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 10.

DE Novel protein.

GN Name=RP23-51G7.3-001;

OS Mus musculus (Mouse);
 OC Buxarota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 NCBI_TaxID=10090;
 OX [1];

RN RNP

RP NUCLEOTIDE SEQUENCE.

Dunn M.;
 DR Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2];

RP NUCLEOTIDE SEQUENCE.

RA Pelan S.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AL731880; CMI125563.1; -; Genomic_DNA.
 DR EMBL; AL669858; CMI125873.1; -; Genomic_DNA.
 DR EMBL; AL731880; CMI125873.1; JOINED; Genomic_DNA.
 DR InterPro; IPR01715; Calponin_act_bd.
 DR Pfam; PF00307; CH; 1.
 DR SMART; SM0033; CH; 1.

DR PROSITE; PS50021; CH; 1.

QY SEQUENCE 1206 AA; 136234 MW; D49618A5DD5D2A82 CRC64;

Query Match 82.9%; Score 4552; DB 2; Length 1206;
 Best Local Similarity 82.3%; Pred. No. 3e-170;
 Matches 925; Conservative 39; Mismatches 74; Indels 86; Gaps 11;

QY 1 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSLSCLIFREGKATDEDMOSLASLVSMQ 60

Db	121 M QYASPMPTQDVKUKEPKVKVNSATLQFSLSCIFLRGKATEDMQLASLMNKQ	D0	1163 KRDALVRDQA E QEKA E DEH L ERTLEQNKG K KEKCALQ 1206
Qy	61 ADIGNLDDFEEDNEDDENR Y NEBEKA K IT-----	RESULT ?	Q12J6_ MOUSE
Db	181 ADIGNLDDFEEDNEDDENR Y NEBEKA K IT T IVNQNL A SSL D QDC I KQAN V SAK 240	ID Q12J6_ MOUSE PRELIMINARY: PRT; 1206 AA.	Q12J6_ MOUSE
Qy	92 -----ELINKUNFLB A OKLAT V NSNPFD P DAE N LPFG D SE R PI T ETASPRKT 145	AC 091ZJ6_	091ZJ6_
Db	241 SASSEBLINTANFLB A OKLAT V NTNP F DE P DT E PT V NE P GD S ----- 287	DT 01-DEC-2001,	integrated into UniProtKB/EMBL.
Qy	146 DS FVNNSNYPKEVQTPQYLPFDEPAAFTKDSPOSTKRKNIRPYDMSKLYADSK 205	DT 01-DEC-2001,	sequence version 1.
Db	288 -----GVQT P QYLNP F DE P ET V MIKOS P STRKRKNIRPYDMSKLYADSK 335	DT 07-FEB-2006,	entry version 19.
Qy	206 TERELD ESNPFP KEVOTPOYLN P DE E PA A FTKDSPOSTKRKNIRPYDMSKLYADSK 335	DE KIAA093-like protein.	Name=Elbp1; Synonyms=AF424697;
Db	206 TERELD ESNPFP KEVOTPOYLN P DE E PA A FTKDSPOSTKRKNIRPYDMSKLYADSK 335	OS Mus musculus (Mouse).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	206 TERELD ESNPFP KEVOTPOYLN P DE E PA A FTKDSPOSTKRKNIRPYDMSKLYADSK 335	OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	OC Muridae; Muridae; Murinae; Mus.
Db	336 S-EBELD ESNPFP KEV K P T -SPNNLV T VO G ET E TR V RK A -----PAPV L 253	OK NEBI_TaxID=10090;	OK
Qy	336 S-EBELD ESNPFP KEV K P T -SPNNLV T VO G ET E TR V RK A -----PAPV L 253	RN [1]	RN
Db	336 S-EBELD ESNPFP KEV K P T -SPNNLV T VO G ET E TR V RK A -----PAPV L 253	RP NUCLEOTIDE SEQUENCE.	RP
Qy	254 PI T GVNL V NT- V SA G COL S TP K PS P IS P V G PK R NA S Q L WCK V TK Y RG V KT N 312	RC STRAIN=C57BL/6J;	RC
Db	394 PK T GV N NT V SA G COL S TP K PS P IS P V G PK R NA S Q L WCK V TK Y RG V KT N 452	RK MEDLINE=22225413; PubMed=12174196; DOI=10.1186/1471-2156-3-14;	RK
Qy	313 FT TSWRNGLSP CAILHHRP D LD I Y K IS N PO D DK I KENN N KAYDGFASIG T SR I LE P SD M VL 372	RA Fuchs S., Resch K., Thiel C., Ulbrich M., Platzer M., Jockusch H.,	RA
Db	453 FT TSWRNGLSP CAILHHRP D LD I Y K IS N PO D DK I KENN N KAYDGFASIG T SR I LE P SD M VL 372	RA Schmitz-John T.; transcription map of the wobbler critical region on mouse	RA
Qy	373 LA PDKLUTW TY Q RA H FS G OB N LV V QI E EN S SS K ST Y KV Y GT E TD N SS O EKF Y AE 432	RT chromosome 11 and the homologous region on human chromosome 2p13.14. ";	RT
Db	513 LA PDKLUTW TY Q RA H FS G OB N LV V QI E EN S SS K ST Y KV Y GT E TD N SS O EKF Y AE 572	RT BMC Genet. 3:14:14 (2002).	RT
Qy	433 L S D L K R RE B LP Q IS G AV D FL S Q D S V U N D S VG E SE H OP D D H LS P ASP Y RT 492	CC copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC
Db	573 L S D L K R RE B LP Q IS G AV D FL S Q D S V U N D S VG E SE H OP D D H LS P ASP Y RT 632	CC distributed under the Creative Commons Attribution-NonDerivs License	CC
Qy	493 K S TE P Q I Q S Q S Q S RT S GS D D P GC I CS N TD S TM Q VL I KK L KA E BT I LS I Y V SD M VL 552	DR EMBL: AF424697; HAL:4806.1; -; mRNA.	DR
Db	633 K S TE P Q I Q S Q S ART S GS D D P GC I SS S TD S SA Q AL S CK R LKAENELSLCVSD M KK 691	DR HSSP; O0102; IJKR.	DR
Qy	553 D M R P P F C I RET S DK L Q T D G I S LE C R S DP S PI K T S LP T SK G YS 612	DR MGII; MGII:2667257; Elbp1.	DR
Db	692 D M R P P F ---LS A Y Q Q L Q T TA H SS M EQ K ME K RS L BR G DL A LT I PK V NS P SK G -- 745	DR InterPro; IPR01715; Calponin_act_bp.	DR
Qy	613 Y S D D L A K K K H SL R Q T ES P PD A RT T HA H SS K VL V OH R LS R BE L K R AR V ILE Q 672	DR PROSITE; PS50021; CH; 1.	DR
Db	746 Y N R D T P T K P C A S I R Q E SD P D A K S T N HA H PN K VA H OH R LS R BE L K R AR V ILE Q 805	DR SMART; SM00033; CH; 1.	DR
Qy	673 A R D A A K G N K H NT T AT P C U R Q LS D Q O DE R ER R Q L R E R A R Q L A ARS Y KM S LS P 732	DR PROSITE; PS50021; CH; 1.	DR
Db	806 A R D A A K G N K H NT T AT P C U R Q LS D Q O DE R ER R Q L R E R A R Q L A ARS Y KM S LS P 865	DR SEQUENCE; P50021; CH; 1.	DR
Qy	733 Y E RNA A AK K K L K R RS G D B ND E NT I BT E RP G F V GG D EL T NT I SD D PE Q NS K 792	DR Best Local Similarity 82.6%; Score 4532; DB 2; Length 1205;	DR
Db	866 Y E RNA A AK K K L K R RS G D B ND E NT I BT E RP G F V GG D EL T NT I SD D PE Q NS K 925	DR Matches 922; Conservative 39; Mismatches 77; Indels 86; Gaps 11;	DR
Qy	793 D A CK K LE V Q V AN S SS A Q V AT S ES S DM K SG T ED P LT E RL O KT E RP N PF V 852	DR	DR
Db	926 D A CK K LE V Q V AN S SS A Q V AT S ES S DM K SG T ED P LT E RL O KT E RP N PF V 985	DR	DR
Qy	853 K O ST V K T Q O LS S Q Y IE N RP M K R Q S I Q E T DK G NE K KA A TT E T O RP S DE V LN K 912	DR 146 DS FVNNSNYPKEVQTPQYLPFDEPAAFTKDSPOSTKRKNIRPYDMSKLYADSK 205	DR
Db	986 K O ST V K T Q O LS S Q Y IE N RP M K R Q S I Q E T DK G NE K KA A TT E T O RP S DE V LN K 1042	DR 288 -----GVQT P QYLNP F DE P ET V MIKOS P STRKRKNIRPYDMSKLYADSK 335	DR
Qy	913 K O ST V K T Q O LS S Q Y IE N RP M K R Q S I Q E T DK G NE K KA A TT E T O RP S DE V LN K 972	DR 206 TERELD ESNPFP KEVOTPOYLN P DE E PA A FTKDSPOSTKRKNIRPYDMSKLYADSK 335	DR
Db	1043 K O ST V K T Q O LS S Q Y IE N RP M K R Q S I Q E T DK G NE K KA A TT E T O RP S DE V LN K 1102	DR 336 S-EBELD ESNPFP KEV K P T -SPNNLV T VO G ET E TR V RK A -----PAPV L 393	DR
Qy	973 AL TRM M O LS L KE H DL R Y V EL N RL A MA I ED M Q T AK R Q B OL L DEL V LN V 1032	DR 337 LA PDKLUTW TY Q RA H FS G OB N LV V QI E EN S SS K ST Y KV Y GT E TD N SS O EKF Y AE 432	DR
Db	11103 AL TRM M O LS L KE H DL R Y V EL N RL A MA I ED M Q T AK R Q B OL L DEL V LN V 1162	DR 453 FT TSWRNGLSP CAILHHRP D LD I Y K IS N PO D DK I KENN N KAYDGFASIG T SR I LE P SD M VL 512	DR
Qy	1033 K O DA L VR D DA E Q A EE H EL T RL O TL N Q K GN M AK E CK T Q 1076	DR 394 PK T GV N NT V SA G COL S TP K PS P IS P V G PK R NA S Q L WCK V TK Y RG V KT N 452	DR

RA Waterston R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RRP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC
 QY 493 KSDTIEPKQSQQSGRTSGSDDPGICNTSDTQAQVLGKKLKARTLESDLYSDKK 552
 DB 633 KSDTIEPKQSQQSGRTSGSDDPGISSTSDSQAALSLGKTR-LKAENLSLDVCSDKK 691
 QY 553 DMSPPFICEETDEQKLQTLDIGSNLKEKEKLNRSLECRSDPESPIKTSISPLTSKLGS 612
 DB 692 DVSP----LSAYEQLQTVAHSSDNEQKGKNEKSRSLECRUDLTDPESPIKTSISPLTSKLGS 745
 QY 613 YSRDIDLAKKCHASLRQTESDPADRTTLNADHSKIVORHLRSQEEKJERAVLQ 672
 DB 746 YNRDIDTPKKECACIQRQTESDPADRTTLNADHSKIVORHLRSQEEKJERAVLQ 805
 QY 673 ARDAALKAGNKHNNTATPCNRQLSDQDDEERRRQLRARQLJAARSGVKNSLPS 732
 DB 806 ARDAFKVQGSKHGSAAPALCSRQLANDQDDEERRRQLRARQLJAARSGVKNSLPS 865
 QY 733 YGEMAAEKLKERSKASGDENDNIEDTNESEIPEGTVGSDELTMELNDLTPTNSKLV 792
 DB 866 YGEMAAEKLKERSKASGDENDNIEDTNESEIPEGTVGSDELTMELNDLTPTNSKLV 925
 QY 793 DLKLLKLEVOPQVANSPSSAAQAVTESSHEDQMGESTEELTRLQLKTERPNPVFS 852
 DB 926 DLRLKGLLEAQPOVANTLPRAQAVTEASBGEBSGVBLRSLQKTERPNPVFS 985
 QY 853 KDTSTRKTQGFSQVIENTPEMKQRSIQBDTKKGNEEKAITTORKUSSEDEVNLKG 912
 DB 986 KDTSTRKTQGFSQVIENTPEMKQRSIQBDTKKGNEEKAITTORKUSSEDEVNLKG 1042
 QY 913 KDTSOVVGHLAALNEQKOIDTRALVEGRYIAMDTSRTEBEAMMOWEFMLVNKN 972
 DB 1043 KDTSOVVGHLAALNEQKOIDTRALVEGRYIAMDTSRTEBEAMMOWEFMLVNKN 1102
 QY 973 ALIREMNQLSLEKEHDERRYELNRELMLAEDWQTEAQKRGREQLLDSVALVN 1032
 DB 1103 ALIREMNQLSLEKEHDERRYELNRELMLAEDWQTEAQKRGREQLLDSVALVN 1162
 QY 1033 KRDALVRDIDDAQEQKAEEDDEHLETLQNGKMKKEEKVVLQ 1076
 DB 1163 KRDALVRDIDDAQEQKAEEDDEHLETLQNGKMKKEEKVVLQ 1206
 RESULT 8
 Q3TV6_HUMAN PRELIMINARY; PRT; 893 AA.
 ID Q3TV6_HUMAN PRELIMINARY; PRT; 893 AA.
 AC Q3TV6_HUMAN PRELIMINARY; PRT; 893 AA.
 DT 24-MAY-2005, integrated into UniProtKB/TREMBL.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein KMA0903 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kalicki J., Johnson D., Harris A.;
 RT "The sequence of Homo sapiens (Human) BAC clone RP11-443F16."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RA Waterston R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RRP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL; AC007098; AAV14789; 1; -; Genomic DNA.
 DR Ensembl; ENSG00000115504; Homo sapiens.
 DR InterPro; IPR01715; Calponin_act_bd.
 DR PF00307; CH; 1.
 DR SMART; SM0033; CH; 1.
 DR PROSITE; PS50021; CH; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 FT 893 893
 SQ SEQUENCE 893 AA; 100446 MW; 88B387A63176A52E CRC64;
 Query Match 80.4%; Score 4414.5; DB 2; Length 893;
 Best Local Similarity 97.5%; Pred. No. 5.4e-16;
 Matches 864; Conservative 6; Mismatches 15; Indels 1; Gaps 1;
 QY 66 LDDFREDEN-DDENRVNOREKAAKITEFLINKLNFDEAKDLATVNNSNPFDDEAELN 124
 DB 8 LSSLDEDQDCIKQANMRSAKSASSETELINKLNFDEAKDLATVNNSNPFDDEAELN 67
 QY 125 PFGDPSERIETAPRKTEDSTONSPNPKVQTYLNPDEPFRVTFIDSPPS 184
 DB 68 PFGDPSERIETAPRKTEDSTONSPNPKVQTYLNPDEPFRVTFIDSPPS 127
 QY 185 TTKRKRIPDMSKVLYADSKTEBEELDENSNPFPKSTPPNNLVNPQBLEFRRVCR 244
 DB 128 TTKRKRIPDMSKVLYADSKTEBEELDENSNPFPKSTPPNNLVNPQBLEFRRVCR 187
 QY 245 KAPAPPVLSPTKGVNENTVAGKDLSTSPKSPISPVPLGKRNENASQSLILWCKEVTKN 304
 DB 188 KAPAPPVLSPTKGVNENTVAGKDLSTSPKSPISPVPLGKRNENASQSLILWCKEVTKN 247
 QY 305 YRGKLTINFTISWNGLSCIAILHFRPLIDYSLNPODIKENKKAVDGASIGSR 364
 DB 248 YRGKLTINFTISWNGLSCIAILHFRPLIDYSLNPODIKENKKAVDGASIGSR 307
 QY 365 LPSPDMVLLAIPDKLTWMTYLQRAHFSQELNVQTFENNSSTKYKGYEDTNSV 424
 DB 308 LPSPDMVLLAIPDKLTWMTYLQRAHFSQELNVQTFENNSSTKYKGYEDTNSV 367
 QY 425 DQEKEYAELSDLKRBPELQOPTGAVDRFLSDQDSSVFVDGVVERSESHOTPDLHSLST 484
 DB 368 DQEKEYAELSDLKRBPELQOPTGAVDRFLSDQDSSVFVDGVVERSESHOTPDLHSLST 427
 QY 485 ASPYCRRTISDTRQKSSQSGRTSGSDDPGICNTSDTQAQVLGKKLKARTLESD 544
 DB 428 ASPYCRRTISDTRQKSSQSGRTSGSDDPGICNTSDTQAQVLGKKLKARTLESD 487
 QY 545 LYNSDKKOMSPPTCEIDEQKLQTLDIGSNLKEKEKLNRSLECRSDPESPIKTSLS 604
 DB 488 LYNSDKKOMSPPTCEIDEQKLQTLDIGSNLKEKEKLNRSLECRSDPESPIKTSLS 547
 QY 605 PTSKLGSYSRDLDAKCHASLRQTESDPADRTTLNADHSKIVORHLRSQEEKE 664
 DB 548 PTSKLGSYSRDLDAKCHASLRQTESDPADRTTLNADHSKIVORHLRSQEEKE 607
 QY 665 RARVLEARRDAALKAKHNNTATPCNRQLSDQDDEERRRQLRARQLJAARS 724
 DB 608 RARVLEARRDAALKAKHNNTATPCNRQLSDQDDEERRRQLRARQLJAARS 667
 QY 725 VKNSELPSYGMEMAKLKERSKASGDENDNIEDTNESEIPEGTVGSDELTMELNDLT 784
 DB 668 VKNSELPSYGMEMAKLKERSKASGDENDNIEDTNESEIPEGTVGSDELTMELNDLT 727

QY 785 PEONSKLVLKLUKKLEVOPOVANSPSSAAQAVTESSEBDQMSGTEDLRTERIQLTTER 844
Db 728 PEONSKLVLKLUKKLEVOPOVANSPSSAAQAVTESSEBDQMSGTEDLRTERIQLTTER 787
QY 845 FRNEVFVFSKDTSTRKTOLOQSFSQYIENREPMKRQRSIQDTRKKGNEBKAITIORKPSE 904
Db 788 FRNEVFVFSKDTSTRKTOLOQSFSQYIENREPMKRQRSIQDTRKKGNEBKAITIORKPSE 847
QY 905 DEVUNKGKEDTSQYVGEALALENEQKIDTRALVALVERKLRYIMDT 950
Db 848 DEVUNKGKEDTSQYVGEALALENEQKIDTRALVALVERKLRYIMDT 893

RESULT 9
Q4SGB9_ TETNG PRELIMINARY; PRT; 1036 AA.
ID Q4SGB9_ TETNG PRELIMINARY; PRT; 1036 AA.
AC Q4SGB9_ TETNG PRELIMINARY; PRT; 1036 AA.
DT 19-JUL-2005, integrated into UniProtKB/TREMBL.
DT 07-FEB-2006, entry version 4.
DB Chromosome 17 SCAR14597 whole genome shotgun sequence.
GN ORName=GSTENG001871101;
OS Tetraodon nigroviridis (Green puffer).
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neorelalosteii;
OC Acanthomorpha; Acanthopterygii; Paracanthopterygii; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TAXID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed-15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costa C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Basiliau C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bleumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Contarneau J.-P., Gouzy J.,
RA Paxia G., Lardier G., Chapple C., McKewan K.J., McElwain P., Bobak S.,
RA Kellis M., Wolf J.-N., Guigo R., Zody M.C., Meilir J., Bobak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Loubard V., Schachter V., Quétier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Scarpelli C.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope, Whitehead Institute for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC - CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.

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CC EMBL, CAE01014597; CAG00313.1; -; Genomic_DNA.

DR InterPro; IPR001715; Calponin_act_beta.

DR Pfam; PF00307; CH; 1;

DR SMART; SM0033; CH; 1;

DR PROSITE; PS5021; CH; 1;

DR SBQENCE; 1036 AA; 114819 MW; C1A8BB29F17262B6 CRC64;

Query Match 41.3%; Score 2265.5; DB 2; Length 1036;
Best Local Similarity 49.1%; Pred. No. 9.1.e-81; Mismatches 188; Indels 235; Gaps 30;
Matches 524; Conservative 121; MisMatch 60

QY 1 MKOYASPMPTQTDVKLKPKPLSKKVSAAQFLQSLSCIFREGKATDEMDQSLASLVSMSKQ 60
Db 32 MKOYASPMPTQTDVKLKPKPLSKKVSAAQFLQSLSCIFREGKATDEMDQSLASLVSMSKQ 91

QY 61 ADIGNLDDEEDDENRVNQBEKAKIT-----ELINKNPLDEAK 105

RESULT 10
Q5PQM3 RAT PRELIMINARY; PRT; 762 AA.
ID Q5PQM3 RAT PRELIMINARY; PRT; 762 AA.
AC Q5PQM3; 762 AA.
DT 04-JAN-2005, integrated into UniProtKB/TREMBL.

Db 92 ADIGNLDDEEDDENRVNQBEKAKIT-----ELINKNPLDEAK 151
QY 106 DLIA-TVNNSPFDDPDAI---ELAPFGDPDSBEPITETASPRKTEDSFYNNSYNPFK--- 157
Db 152 EASPMSTNFDPDDSLHPRHNPFDPDMERAPQPNSDLPENDHDSSNPEDP 211
QY 158 --EVOTPOYLNPDEPEAFVTK--DSDPOSTKRKNTRPVDSKLYADSSKTYEEBDELDE 213
Db 212 EPELQTG--NPFDEPDQDLPDPBPFPKPRORGVYFPVNDMSKLYADNVNEDELDD 269

QY 214 -----SNPYEPKSTPPRNVLVPVQELFTERVYKRPAP 249
Db 270 FTOLFLGCNVRSERNMCHFCISLRSNPYPYKISSPAKPVQEG-PSLMSSQRARRPP 328

QY 250 PVLSPKTG-----VIAENTUSA--GKD--STSP-----K 275
Db 329 PSSPGKRPSPASKPSSVPDREOALAVGSPSPYTAIGCRLASSRPLQGAVISLARK 388

QY 276 PSPITPSPVLRKNAQSSLVWCKEVTRVYKRVKINTFTSRNGLSPFCALIHHFRDLI 335
Db 339 PSPIPSPLGKPKNAQSSLVWCKEVTRVYKRVKINTFTSRNGLSPFCALIHHFRDLI 448

QY 336 DYKSLNPDPDIKENKKADGFASIGTRILRPLPSDMVIAIPDKLTWVUMLYDRAHSGQ 395
Db 449 DYKSLNPDPDIKENKKADGFASIGTRILRPLPSDMVIAIPDKLTWVUMLYDRAHSGE 508

QY 395 DYKSLNPDPDIKENKKADGFASIGTRILRPLPSDMVIAIPDKLTWVUMLYDRAHSGQ 452

Db 509 ELNVVQIRANSSTSYKTYGDPFTDNASIDQKFYAZNDVQGRQVNAQPVUTASGNS 568

QY 453 LSQDDSV-----FVNDGSGESESEHOTPDHLSPTASPYCRTKSDETEPKSQSSGR 507

Db 559 TKNEGDGPKADCNVDKAVTKTGQ---OSSPPVESP---RTVGTWSVDSQA--- 618

QY 508 TGSDDPPIGCSNTNSTDSTQVQILGKRLKAETBLSDIYVSDKKDMSPPFICRETBDQK 567

Db 619 TPASEBERG-----SLTKANTIDLSELSPORERE----- 645

QY 568 LQTLIDGSNLKEKLNCSR---SLECTSDPSPPIKTSLSPT---SKLGYSYRDLA 620

Db 646 -----MEKEQQKOKKVGEETNEGTPESPSPGRGPSSPPHOMQGLGFSNRDADLI 696

QY 621 KKQHASLQTESDPADDET-TLNHAD-----SSKIVOHRLSROELKERR 667

Db 697 KKCBASLHSSESPADSPCSPPNHTPPQQBPTPVTVTSLSAEKVLRSQBELKERR 756

QY 658 VILLEQARDUALKAGNKNTNTATPCIN---RQSLDQOBBERRQLRERARQLTAEARASGV 725

Db 757 LILHQARIDAMAKSNKONPDSANAANISTTVCDERDAERRQLRERARQLIAEASGV 816

QY 726 KNSLPLSGEMAJAEKLK-ERSKASGDEDNTISIDTNHEIPCFVUGGGDELNLENDDT 784

Db 817 KNSLPLSGEMAJAEKLK-ERSKASGDEDNTISIDTNHEIPCFVUGGGDELNLENDDT 857

QY 785 PEONSKLVLKLUKKLEVOPOVANSPSSAAQAVTESSEBDQMSGTEDLRTERIQLTTER 844

Db 888 -----SERGIGAATQSHRE----- 873

QY 845 FRNEVFVFSKDTSTRKTOLOQSFSQYIENREPMKRQRSIQDTRKKGNEBKAITIORKPSE 903

Db 874 VRNEVFVFSKDTSTRKTOLOQSFSQYIENREPMKRQRSIQDTRKKGNEBKAITIORKPSE 933

QY 904 PEONSKLVLKLUKKLEVOPOVANSPSSAAQAVTESSEBDQMSGTEDLRTERIQLTTER 951

Db 934 EBSYLNKGKEDTSQYVGEALALENEQKIDTRALVALVERKLRYIMDT 981

DT 04-JAN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 12.

DB LOC309169 protein.
 GN Name=LOC309169;
 OS Rattus norvegicus (Rat).

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 RN [1] -TaxID=10116;

RP NUCLOBOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsunaga K., Farmer T., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boksa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarino P.H.,
 RA Richards S., Worley K.C., Haize S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Falley J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalak R.A., Smalius D.E.,
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP NUCLOBOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RL Submitted (BSC-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL: BC087115; AAH87115.1; - mRNA.
 DR Ensembl: ENSRNOG00000020788; Rattus norvegicus.
 DR InterPro: IPR001715; Caponin_act_bd.
 DR Pfam: PF00307; CH; 1.
 DR SMART: S00033; CH; 1.
 DR PROSITE: PS50021; CH; 1.
 DR SEQUENCE 762 AA; 84105 MW; 1249PDT0B4BB886C CRC64;

Query Match 21.0%; Score 1154.5; DB 2; Length 762;
 Best local similarity 30.0%; Pred. No. 2.1e-37;
 Matches 325; Conservative 104; Mismatches 205; Indels 449; Gaps 20;

QY 1 MKQVYASPMPPPTDVKLKKPLSKKVMSALQPSLSCIPIREGKATBDQMSLASLVSMKQ 60
 120 LAQHAGPVPQAVQPLRLKSKVKVHQHSLTSLGVLRGRATDDMOSLASLVS 179

QY 61 ADIGLDDDEEDDDENRWNQBEKAAKTTELINKNFDDEAEDLATWNNSNPFDDPDA 120
 180 SDVGALDDPABRSDEE----- 194

Db 121 AELNPFGDPDSBRPITETASPRKTEEDSPYNNSYNPKEVQTYINPDEPEAFTIKDS 180
 195 -EANGPGAFB-----VRAG 207

QY 181 PPOSTPKKRNPTRPVPMKSYLYADSSCTTREBRBLDSNPYPYKSTIPPNNUVNQYBLER 240
 208 GPOSDRSREL-----KTLCEBEDGE-----IOPQO----- 233

QY 241 RVKKGAPAPVLPSPKTPKGVLNENTWSAGKOLSTSKPSPIFSPVILGRKPMASQSLIVWCKE 300
 234 - -----AAARP-----SSAEDTSCAPAPSALVS-----SSQSLEWQCB 266

QY 301 VTKNYRGVKITNFSTSWRNGLSFCAILHHRPDLTDYKSINPODTCENRKAYDGFASTG 360
 267 VTGKJRGVCINTNFTSWRNGLAFCAILHHRPDKDIDSFLPLNIKQNNQAFDGPALG 326

Db 327 VSRLIPLPDMDVLLSPVDPKLIVMTYLCQIRACFTGQBLQLVOLEGGGSGTYRVNAQQSL 386

QY 420 --TNSSDOEKFPAELSIKREP-BLOOPISGAVDPLSODDSVFUNDGSVGSESEHQT 475
 Db 387 PDCLANAGDIAQRLRHGAARASTERKEAVNRTGAIKPVAASRDTDLGSSKDGRAEVAQRA 446
 QY 476 PDDHLSPLSTATSPYCRTKEDTEPQSQQSRSRGTSGSDRGICSNSTDSTQVQVLGKRRU 535
 Db 447 ----VPOEASSDGPRASTSPP-WVPTEGLINGVGAPASVSV---- 484

QY 536 KARTULBLSDLVYSKDKKDISPPECTERUBQKLTLDIGSNLREKLENSRLCRSDPS 595
 Db 485 ----- 528

QY 499 PP-----PRAKOSFSHYRADLIKRSRSLRNS----- 528

QY 566 LSROBELKERARVILLEQARRDAALKAGKNGKNTNTATPFCNRQLSDQOBERRROLRER 715

Db 529 ----- 528

QY 716 OLIABARSGYTKMSLPSYCGEMAELKLRSKASGENDNIEIDTNEIPEGFYVGGDEL 775
 Db 529 ----- 546

QY 776 TNLENDLDPBQONSKLVDKLUKLULEVQPQVANSPSSAQAKVTESSBQDMKSGTEDLRT 835
 Db 547 SGA---VBGPNPSSLDGTSLTATAPOOPPSGHP----- 578

QY 836 ERLQXTERFRNPVVFSKDSTVRKTQLOSFQXYTENRPEMKRQSIQDITKKGNNEKAII 895
 Db 579 -----TEBSRPNP----- 586

QY 895 TETORKPSIDEVNLKGFFKDTQSYVNGELALALENEOKOIDTRAALVEKURYLMDTGRIITE 955
 Db 587 -----GEEAGQORFDQTSQVCAELQALEQBGQGDGRANEVEKQURSLMESGARNL 638

QY 956 ERMAMQHFMUMLVKNKALIRRMQMSLJEKDLERYLERVELRMLAIDWQKTA 1015
 Db 639 QEBLIOEFITLVIKNAIRRQDOLQOLQEDOLEPDRERBLRMLAIEEWKQTA 698

QY 1016 QKRBQBLIILDEVALVNLKEDALYRDLQDQBQABEDEHLERTLLEQNQKMAK---KREK 1072
 Db 699 QHREBQBLIILDEVALVNLKEDALYRDLQDQBQABEDEHLERTLLEQNQKMAK---KREK 758

QY 1073 CVL 1075
 Db 759 CTL 761

RESULT 11
 Q93J97_MOUSE PRELIMINARY; PRT; 874 AA.
 ID Q93J97_MOUSE
 AC Q93J97;
 DT 01-JUN-2001, integrated into UniProtKB/TREMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DB Tangerin B (LOC11461 protein).
 GN Name=Kcnk7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 RN [1] -TaxID=0090;

OX NCBI_TaxID=10090;
 RN [1] : : :
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RA Melichar J.M., Noegel A.A., Korenbaum E.;
 RL Submitted (SSP-2000) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: AF030509; AAK32112.1; -; mRNA.
 DR HSSP: Q01082; 1BKR.
 DR Ensembl: ENSMUSG0000024937; Mus musculus.
 DR MGI: 1341841; Kcnk7.
 DR GO: 00116021; C:integral to membrane; RCA.
 DR GO: 0016020; C:membrane; RCA.
 DR GO: 0005267; P:potassium channel activity; RCA.
 DR GO: 0006813; P:potassium ion transport; RCA.
 DR InterPro: IPR001715; Calponin_act_bd.
 DR Pfam: PF00307; CH; 1.
 DR SMART: SM00033; CH; 1.
 DR PROSITE: PS50021; CH; 1.
 SQ SEQUENCE: 759 AA; 83948 MW; 8770323D25E707B4 CRC64;
 Query Match 20.6%; Score 1131; DB 2; Length 759;
 Best Local Similarity 29.8%; Pred. No. 1.8e-36;
 Matches 325; Conservative 107; Mismatches 190; Indels 470; Gaps 25;
 QY 1 MKQVASYPMPTQTDVKLKFKPKISKVVAALQPSLSCIFREGKATDEDDMOSLASILVSMQ 60
 Db 120 LAHHAGHPVPAQVPLRKLRIKEPSKVTVHAEELSLTISGVLLREGRAATDDMOSLASILMSVKP 179
 QY 61 ADIGMLDDEPFDNEDDENRNQBEIKAKITTEBLINKNLFLDARKDLATWNNTNPDDPA 120
 Db 180 SDVGNDLDRFASDES----- 194
 QY 121 ABLNPGDPDSBEPITETASFRKTEDSFVNNSYNPKFEVOTQXLNPFDEPEAFWIKOS 180
 Db 195 -EANGRGPAE----- 207
 QY 181 PPOSTKRKNIPRVDMSKYLAQSKTKEEBELIDESSNPYFPSPKSTPPRNPNLYNPVOLER 240
 Db 208 GPQS-----DLISREL-----KTCCEBDEGH-----IRPQQ----- 233
 Qy 241 RVRKKAPAPPVLSPTKGVLNEINTSAGKOLTSKPSPPIPSPVLRKPNASQSLIVCKE 300
 Db 234 -----AAARE-----SSAEP-----TSPAP-----PTL-----VASSQSLWCB 266
 QY 301 VTKNYRGVKITNFITSWRNGLSPCALHLHERRDLDYKSNIPQDITKENKKAYNGFASTG 360
 Db 267 VTINGRGVCTINFTSWRNGLAFCAHLHFPDKDIDSPUDPLIKNNQKAFOGAALG 326
 QY 361 ISRLLEPSDMVLLAIPDKLUTMITYQTRAHPSGQBLYNVIQIBERNNSKSTTYKVNTYT 420
 Db 327 VSRLLEPADWVLLSVFDKLIVMTICQIRACTGIGOBLOLVOLEGEGGGSGTYRVNAQSL 386
 Qy 421 NSSVQDKFVYAEELSOKREPLQPI-----SGAVDPLSODDSVFSVNDSGVSESES 471
 Db 387 PDCUA----GDAQRLRBRGAETVTEPKAVNRTGTAIPKVASRDTDISCSKIDGRB- 441
 QY 472 EHQPDDHLSPTASPYCRTKSDEPOKSQSQSSGRTGSDDP----GICSNSTDQAQ 526
 Db 442 -----VAQEAIQPAAPTDEPRAESTTPVPAEGLVWYGAS--- 478
 QY 527 VLLGKCRRLKAKETBLSDLVSDKCKMDAPPICBETDEQKLQTUDIGENLEKLEKLNRS 586
 Db 479 --GGVRLRS----- 486
 QY 587 SIECRSDPSPPIKKSLSPTSKGYSYSRDLAKKHKHSRQTESPDADRTLNHADH 646
 Db 487 SVNGEAGPVPP-----PRAGSFHVRAUDLCKERSLR----- 521

QY 647 SSKIIVQRHLSRQEELKERARVLLQARRDAALKAGNKINTATPPCNRQLSDQDEER 706
 DR 522 ----- 532
 DR 707 RRQLRERAROLIAEARSGVNMSELPSYGENAAEKLKERSKASGIDBENDNIBIDTNBEPIC 766
 DR 533 -----SGAANGAGPA-GFCAVE----- 548
 DR 767 FVVGCGDBLTLNLENDLTDTBQNSKLVDLKLKLIVQPOVANSPPSSAQAKAVTSESQDM 826
 DR 549 -----GPNPASPDANTPLPAPVHQOPPG 572
 DR 827 KSGTSDLRLTERLQKTERFRNPKVPSKDSVTRVKIQTQLQSQYIENRPMKRSIQEDTK 886
 DR 573 PPPT----- 591
 DR 887 KGNEBKAATETORKPSDEDEVLNKGPKTSQYVVGBLAENEQKIDTRALYVRLRY 946
 DR 592 -----FQDTSQYVCAESLOALQECOCQDQGKRAEVEKQURS 626
 DR 947 LMDTGTRNTTREBAMMQENMLVNKGKALIRRMMQNLSLKEDLRRYVILNRLRAMLA 1005
 DR 627 LMEGANRQLQEVLIQEWFTLVNKGKALIRRQDOLQOLITEQDLERLRLFLLSRLRAMLA 686
 DR 1007 IEDWQKTEAKRKGQDILDELVALVNRKDALVRDQKQASBDEEHILTELEONKGK 1066
 DR 687 IEWQKTVQAOHREOULLBLVLSVNQDULVRLDQGERTIALBEDERLRLERGLBQRRK 746
 DR 1067 AK---KEEKCVL 1075
 DR 747 SRQLSRRERCTL 758

RESULT 13
 Q99MS5_MOUSE
 ID Q99MS5_MOUSE PRELIMINARY: PRT: 771 AA.
 AC Q99MS5;
 DT 01-JUN-2001; integrated into UniProtKB/TYMBOL.
 DT 01-JUN-2001; sequence version 1.
 DT 07-FEB-2006; entry version 17.
 DE Tangerin C'.
 GN Name=Kcnk7;
 OS Mus musculus (Mouse).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/C;
 RA Melichar J.M., Noegel A.A., Korenbaum E.;
 RL Submitted (SSP-2000) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: AF030509; AAK32112.1; -; mRNA.
 DR HSSP: Q01082; 1BKR.
 DR Ensembl: ENSMUSG0000024937; Mus musculus.
 DR MGI: 1341841; Kcnk7.
 DR GO: 00116021; C:integral to membrane; RCA.
 DR GO: 0016020; C:membrane; RCA.
 DR GO: 0005267; P:potassium channel activity; RCA.
 DR GO: 0006812; P:cation transport; RCA.
 DR GO: 0006813; P:potassium ion transport; RCA.
 DR InterPro: IPR001715; Calponin_act_bd.
 DR Pfam: PF00307; CH; 1.
 DR SMART: SM00033; CH; 1.
 DR PROSITE: PS50021; CH; 1.
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 Best Local Similarity 29.8%; Pred. No. 2.6e-36;

- RP NUCLEOTIDE SEQUENCE
 RN STRAIN=C57BL/6J; TISSUE=Ovary;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT "Genome Network Core Team) and the FANTOM Consortium;"
 RL "Antisense Transcription in the Mammalian Transcriptome.";
 RN [4]
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 MEDLINE=22356863; PubMed=12456851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikido I., Otao N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beiel K.W.,
 Blake J.A., Bradt D., Brusic V., Chothia C., Corrani L.E., Cousins S.,
 Dalla B., Drigani T.A., Fletcher C., Frazer A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Gough J.,
 Grimmond S., Gustincich S., Hikawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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 Nasashima T., Numata K., Okido T., Pavani W.J., Partea G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Reeder J.C., Reed J.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultan R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner D., Wahlestedt C., Wang Y., Wattanabe Y., Wells C.,
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang J., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Wakai K., Kawai J., Aizawa T., Fukuda S.,
 Hara A., Hashizumi W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
 Yasunishi K., Hayashizaki Y., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 Nature 420:563-573 (2002)."
 RN [5]
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 MEDLINE=2105660; PubMed=11211851; DOI=10.1038/35055500;
 RA Kawaji Y., Shigenobu S., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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 Saito T., Okazaki Y., Nojihori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cabavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matuo T., Mazzoni T., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stuhli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,
 RA Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maslima M., Mazzarulli J.J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasuki H., Sato K., Schoenbach C., Seya T., Shitara Y., Storch K.-F.,
 RA Suzuki K., Toyo-oka K., Wang K.H., Weitz C., Whittaker L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL "Genome Res. 10:1617-1630 (2000)."
 RN [6]
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 MEDLINE=20499574; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayashizaki Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL "Genome Res. 10:1617-1630 (2000)."
 RN [7]
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 MEDLINE=2053013; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibusawa K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kondo H., Akiyama T., Nishii K., Nishimine T., Tachiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL "Genome Res. 10:1757-1771 (2000)."
 RN [8]
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RA Adachi J., Alzaga K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Kura A., Hashizume W., Itoh M.,
 RA Hayashida K., Hayakawa N., Hiramoto K., Hirokawa T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kuroda T., Kasumida K.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sakai D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagami A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi K., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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 CC EMBL; AK087817; BAC40012.1; - ; mRNA.
 DR HSSP; Q01082; IBKR.
 DR InterPro; IPR01715; Calponin_act_bp.
 DR Pfam; PF0307; CH; 1.
 DR SMART; SM0033; CH; 1.
 DR PROTEB; PS50021; CH; 1.
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 Best Local Similarity 30.2%; Pred. No. 1.4e-34;
 Matches 323; Conservative 109; Mismatches 257; Indels 382; Gaps 27;
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 Query Match 19.7%; Score 1082; DB 2; Length 723;
 Best Local Similarity 30.2%; Pred. No. 1.4e-34;
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 DB 2 VLLREGGRATDDMOSLISLMSVRSQDSVNDLFRSDERBRANGPAPVTRGQPSDLSR 61
 QY 96 KLNFLDEBARDLDTWNSNFDDPAEALNPFGQPD-SRPIPEASPRKTEDSFYNNYN 154
 DB 62 EKLTCLCE-BEDEGHIR----FOQAARAPSSAEDTSAPVSAAPVTA----- 104
 QY 155 PPKEVQTPQVINYDPDEPRAFKTQSPQSTKRKNIRPVDMSKVLYAASSKTERELBS 214
 DB 105 -----FRGQDSEPARAITGSGVG----- 130
 QY 215 NPFTVEPKSTPPPNLVLNPVOBLETERRVKRPAAPPV-----LSPKTVGLNT 263
 DB 131 PP--ETRSTCQPGTMVPP-APRLRKGSDAASSPPVCSGDEVPNTSBDPPGMSGCR 186
 QY 264 VSA-----GKDL-STSPKSPRSPVPGKRPVASQSLWCKEVTKYRGVKTNTS 316
 DB 187 TOAQTSORGTEAHEARPDPDIEAPTL--VSSSQSLIEWCQBTVCNTSYRGVCITNFTS 243
 QY 317 WRNGLSPCAILHHRPDLIDYKSINPQDIKENKKAYGPGASTIGISRLRPSDMVLLAIP 376

- RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfleiffer B.D., Db
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abrol J.F., Agbayani A., An H.-J., Andrew-Pfankoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
 RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier A.,
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 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischnann W.,
 RA Fosler C., Gabrieleian A.E., Garg N.S., Gebart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Inegwam C.R.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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 RA Markoulou G., Mishina N.V., Moarry C., Morris J., Mosherfi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyj D.M., Nelson D.L.,
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 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamas I., Simpson M., Skupski M.P., McPherson D.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
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 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adamm W., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Many D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Soderzen B.J.,
 RA Svirskas R., Tabor P.E., Wan K.C., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.B.,
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Crosby M.A., Mungall C.J., Matthes D., Prochnik S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallei R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
 RA NCBI_TaxID:7227;
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 RA MEDLINE=019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallei R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
 RA NCBI_TaxID:7227;

RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase;
 RL Submitted (JAN-2006) to the EMBL/GenBank/DDJB databases.
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 EMBL: AB003804; AAC57918.2; -; Genomic_DNA.
 HSSP: Q01082; 1BKR.
 FLYBASE: FBgn0034100; CG15609.
 DR InterPro: IPR007175; Calponin_act_bp.
 DR Pfam: PF00307; CH; 1.
 SMART: SM0033; CH; 1.
 PROTE: PS50021; CH; 1.
 DR Chaperone.
 KW SEQUENCE 987 AA; 111331 MW: D1B74FF2053AD0CE CRC64;

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 Best Local Similarity 28.2%; Pred: No. 3.2e-34;
 Matches 324; Conservancy 178; Mismatches 291; Indels 357; Gaps 39;
 Matrices 344; Conservative 178; Mismatches 291; Indels 357; Gaps 39;

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 121 WKKYASIESSTQOSFTLSLKPSKKCTAASLILITCISVFLRKGRKATBDMOSLVSKMSVN 180

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 181 NDVAPLUDDBLIDPDLCGFSBTIDNFENDFTQOCUHMTSLSNGCIDVATPOSVPSLSBDPTP 240

QY 90 ITELINKLNFDDEAKDLATVNSNPDDPDAEKLNPFGDPS-----EBPI-- 135
 241 LAESENPLHF---ELODGKORERANKDLPLPAGSGSSGASESLKTPNGIQLHWNPOTPIK 298

QY 136 -TETASPRKTE-DSFYNNSYNPKEVQTPQYLPDEPE-----ARTVIKOSPPQS 184
 299 PDEVKPKQFVPEVSLASKTNEDFKRNTSIFPLEPNVNNDVKPKKGKRALPFTEKD-EQD 357

QY 185 TTKNQIRPVMDISKVLYIADSKCTTERELDRENPPVYERKSTPPNNLVNPVQELET-----240
 358 LRVESVKE-DTWTKT-GDNST-TKEPKKEESQSQSKDASSVWPSAKRPELQPLNLCKSYEP 415

QY 241 -RVRKKAPEAPPVLSPLSKTGVLENNTSAGKOLSTSKPS---PIPSVPLGRKPNAQSLL 295
 416 SQTRESAPV-----ASVNE--SIGCFSTCSLNNLSKPVKIVI-KENTPGQDIL 465

Db 295 WCKCKEVTKNTRGVKUTNFTWSWRNGLSPFCMILHHRPDLIDYKSLNPQDTKENNKAYDG 355

QY 466 EWCKEVTKDYPNVKNTNLTSWRNGMAFCAIHHFVPELIMSKLSAHDVGNCRIGFDA 525

QY 356 FASG1SRLIEPSPDMVILAPDKLTWMTYIQIRAHPSGELVNYQIBENNSKSYKVN 415

Db 526 AELSGIPRVRPDRMLTVDPDKLAMTYLQMLRAHTPSKQKQKLBQIGSTADESSYVIGD 585

QY 416 YKDTINSSVDOBKPKFVAKLSDJKREPLQQPSIGAVDPLSODSVFVNDSGWGESEHQT 475

Db 586 YKSD-NLSQNRINPSKPSLHLQNSPDRBENG-----MKSEQLS 625

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Db 674 TPPQBSLDKGSQPG-----GKNSII-TTIDPQR-----ASRI 705

QY 656 LSROBEKLKERARVVLLEQARRDAALKAGKNTNTATPCURQLSDQQDBERRQRBAR 715
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 707 LTRKHMSEGAKLUMEMERKUN-----KTSANDPERQQLLEQAR 746

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Db 785 EHAKULEKPGSFSHRLSDPKV-----LOSFNAIVE-----RVSPKHEKR 825

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Db 861 MGGNPRTETREEQULSQWFTLUNKNALLARQMONLNTLQBKDLERKTYMLNQSLRACG 920

QY 1007 IEDWOKTEAQKREBQOLLDLVALVNUKRDALVROLDADAQSKQAERBDEHILERTLQBNKGK 1066
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 921 VEDWAKTEEVOREKERULLBLMTVDKRQOLVQHLNQB-LAEDDQEARKLKH--VDI 977

QY 1067 AKKEKCVLQ 1076

Db 978 SAEKOKCVLQ 987

Search completed: May 20, 2006, 17:14:41
 Job time : 332 secs

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xx
 CC The invention relates to human cytoskeleton-associated polypeptides (CYSKP) and their associated polynucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell proliferative disorders (such as cancer, actinic keratosis, arteriosclerosis, cirrhosis, hepatitis and psoriasis), autoimmune/inflammatory disorders (such as, asthma, atherosclerosis, osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus and anemia), vesicle trafficking disorders (such as hypercholesterolemia, diabetes insipidus, Graves' disease and goitre), gastrointestinal disorders, priion diseases, neurological disorders (such as epilepsy, stroke, cerebral neoplasma, Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis and other motor neuron disorders), cell motility disorders, reproductive disorders (such as endometriosis and polycystic ovary syndrome), muscle disorders (such as myoclonus, migraine, hypertension, hypoglycaemia, myocardial infarction, epilepsy and muscular dystrophy), spinal cord diseases, central nervous system disorders (such as Down syndrome and cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
 CC Sequences AAU74330-AAU74363 represent human CYSKP of the invention.
 xx
 SQ Sequence 1076 AA;

xx

Query Match 99.9%; Score 5486; DB 5; Length 1076;
 Best Local Similarity 99.9%; Pred. No. 0; Matches 1075; Conservativeness 1; Mismatches 0; Indels 0; Gaps 0;

QY

1 MKQYASPMPTQDVKLKEPKLKKVSAALQFSIASCIFURGKATDEMQSLASIVSKQ 60
 Db 1 MKQYASPMPTQDVKLKEPKLKKVSAALQFSIASCIFURGKATDEMQSLASIVSKQ 60
 QY 61 ADIGNLDDPFEEDNDDDEENRVOHQEEKAAKITELINKNLFDEAKDLATVNNSNPDDDA 120
 Db 61 ADIGNLDDPFEEDNDDDEENRVOHQEEKAAKITELINKNLFDEAKDLATVNNSNPDDDA 120
 QY 121 ARKANPFGDPSSEPIETASPRKTEDSFYNNSNPKEYQTPOYLNPFEPRAFTIDS 180
 Db 121 ARKANPFGDPSSEPIETASPRKTEDSFYNNSNPKEYQTPOYLNPFEPRAFTIDS 180
 QY 181 PROSTKAKWIPDMSKVLYADSSKTEERBLDESNPFPKSTPPPNVNPQBLEER 240
 Db 181 PROSTKAKWIPDMSKVLYADSSKTEERBLDESNPFPKSTPPPNVNPQBLEER 240
 QY 241 RVKRKAPAPPVLSFKTGVNLNTVSAGKOLSTSPKPSFIPSPLVGRKPNASILVWCER 300
 Db 241 RVKRKAPAPPVLSFKTGVNLNTVSAGKOLSTSPKPSFIPSPLVGRKPNASILVWCER 300
 QY 301 VTKNYRGVQLTINFTSWRNGLSCAIIHFRPDIDYKSINPODIKENNKAVDGASIG 360
 Db 301 VTKNYRGVQLTINFTSWRNGLSCAIIHFRPDIDYKSINPODIKENNKAVDGASIG 360
 QY 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHPSQBLNVQIEENNSKTYKIGNYEDT 420
 Db 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHPSQBLNVQIEENNSKTYKIGNYEDT 420
 QY 421 NSSVDOQEKEYAETSDLKREBPELOOPISGAVIDSODDSVFNDSGVGESESHTOPDHL 480
 Db 421 NSSVDOQEKEYAETSDLKREBPELOOPISGAVIDSODDSVFNDSGVGESESHTOPDHL 480
 QY 481 SOSTASPICRRTSDETEPKSOSSGRGSDDPGICNTSDTOAQVILGKRKLKARTL 540
 Db 481 SOSTASPICRRTSDETEPKSOSSGRGSDDPGICNTSDTOAQVILGKRKLKARTL 540
 QY 541 ELSLDLYSDKKKOMSPPRICEENDBKQKQTLIGSNEKEKLENSLSCRSPESPPIK 600
 Db 541 ELSLDLYSDKKKOMSPPRICEENDBKQKQTLIGSNEKEKLENSLSCRSPESPPIK 600
 QY 601 TSISPTSLKGYSISRDLIAKKGHASLROTESDADRTLNHDHSKIVQVRLLSRQB 660
 Db 601 TSISPTSLKGYSISRDLIAKKGHASLROTESDADRTLNHDHSKIVQVRLLSRQB 660
 QY 661 ELKERARVILLEQARRDAALKAGNKHNTNTATPCNCNQLSDQODBERRQLRERQIATAE 700

Db 661 ELKERARVILLEQARRDAALKAGNKHNTNTATPCNCNQLSDQODBERRQLRERQIATAE 700
 QY 721 ARSGYKMSLPSGEMABKLKERSKASGDENDNITEINNEPEGFWGGGBLTLNEN 780
 Db 721 ARSGYKMSLPSGEMABKLKERSKASGDENDNITEINNEPEGFWGGGBLTLNEN 780
 QY 781 DLDTPEQNSKLVDLKLUKLEVOPQVANSPPSAQKAYTTESSQDMKGCTEDLTERIQLK 840
 Db 781 DLDTPEQNSKLVDLKLUKLEVOPQVANSPPSAQKAYTTESSQDMKGCTEDLTERIQLK 840
 QY 841 TTERPRNPVUFSKDSTVRCTQLOFSQJENRPEMKRSIQDTRKKNEEKAITEQR 900
 Db 841 TTERPRNPVUFSKDSTVRCTQLOFSQJENRPEMKRSIQDTRKKNEEKAITEQR 900
 QY 901 KPSADEVNLKGKDTSQTVNGEALLENQKQDTRAALVEKLYMLDTGRATEESEM 960
 Db 901 KPSADEVNLKGKDTSQTVNGEALLENQKQDTRAALVEKLYMLDTGRATEESEM 960
 QY 961 MQENFMFLANKCNALIRRNQSLAKENDLERYELLNLRELMLATEDWQKTBKRE 1020
 Db 961 MQENFMFLANKCNALIRRNQSLAKENDLERYELLNLRELMLATEDWQKTBKRE 1020
 QY 1021 OLLUDDELVALVNKRDALRDQEQKFEEDSHLERLTBONIKGMKREKCVLQ 1076
 Db 1021 OLLUDDELVALVNKRDALRDQEQKFEEDSHLERLTBONIKGMKREKCVLQ 1076

RESULT 2

ADL13160
 ID ADL13160 Standard; protein; 1076 AA.
 XX
 AC ADL13160;
 DT 06-MAY-2004 (first entry)

DB Human steroid-induced C3A liver cell protein #134.
 KW Hepatotropic; Gene therapy; Wilson disease; liver disorder;
 KW steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
 OS Homo sapiens.

XX
 PN US6673549-B1.

XX
 PR 06-JAN-2004.

XX
 PA (INCY-) INCYNE CORP.

XX
 PI 12-OCT-2001; 2001US-00976594.

XX
 DR 12-OCT-2000; 2000US-0240409P.

XX
 PA (INCY-) INCYNE CORP.

XX
 PI Furness LM, Buchbinder JL;

XX
 WPI; 2004-060610/07.

PT Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid treatment.

XX
 PT Disclosure; SEQ ID NO 889; 141pp; English.

CC The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecule or compounds to identify a ligand that specifically binds a cDNA comprises: combining

CC (cyskp) and their associated polynucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell proliferative disorders (such as cancer, actinic keratosis, arteriosclerosis, cirrhosis, hepatitis and psoriasis), autoimmune/inflammatory disorders (such as, asthma, atherosclerosis, osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus and anemia), vesicle trafficking disorders (such as hypercholesterolemia, diabetes insipidus, Graves' disease and goitre), gastrointestinal disorders, priion diseases, neurological disorders (such as epilepsy, stroke, cerebral neoplasma, Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis and other motor neuron disorders), cell motility disorders, reproductive disorders (such as endometriosis and polycystic ovary syndrome), muscle disorders (such as myoclonus, migraine, hypertension, hypoglycaemia, myocardial infarction, epilepsy and muscular dystrophy), spinal cord diseases, central nervous system disorders (such as Down syndrome and cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
 CC Sequences AAU74330-AAU74363 represent human CYSKP of the invention.
 xx
 SQ Sequence 1076 AA;

CC the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cdk and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human protein which is differentially expressed in steroid-induced C3A liver cells. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPRO at seqdata.uspro.gov/sequence.html.

XX Sequence 1076 AA;

Query Match 99.9%; Score 5486; DB 8; Length 1076;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1075; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKQVQASPMPTOTDVKUKPKPSKPKVVAALQFLSCLSPCILRAGKATTDMDMOSLAVSMKQ 60
1 MKQVQASPMPTOTDVKUKPKPSKPKVVAALQFLSCLSPCILRAGKATTDMDMOSLAVSMKQ 60
Db 61 ADIGMUDPFDDEDDENRNRNQEBKAKUTPLINGNFUDERAKDALTINSPNDPDA 120
Db 61 ADIGMUDPFDDEDDENRNRNQEBKAKUTPLINGNFUDERAKDALTINSPNDPDA 120
QY 121 AELNIPFGDPDSSEPIETASBRKTEDSFYNNNSYNPPKEVQTPQYANPFDREAFVTKDS 180
121 AELNIPFGDPDSSEPIETASBRKTEDSFYNNNSYNPPKEVQTPQYANPFDREAFVTKDS 180
QY 181 PPOSTRKRNTRPVDSKYLADASSKTREREDDESUPPYBCKSTPPENNLPVQILTER 240
181 PPOSTRKRNTRPVDSKYLADASSKTREREDDESUPPYBCKSTPPENNLPVQILTER 240
Db 241 RVKRKAPAPPYLSPKGVLMENTVSAGKDLSTSPPSISPPVLRKPNASQSLIWWCKE 300
Db 241 RVKRKAPAPPYLSPKGVLMENTVSAGKDLSTSPPSISPPVLRKPNASQSLIWWCKE 300
QY 301 VTKNTRGVKLTNTFTSWRNGISFCATLHHRFPDLIDYKSJNPQDKKENKKAYDGAFASIG 360
301 VTKNTRGVKLTNTFTSWRNGISFCATLHHRFPDLIDYKSJNPQDKKENKKAYDGAFASIG 360
Db 361 ISRLLPBSPDMVTLAIPDKLTWNTLYQIRAFPSGOBLANVQIBRENSKSTKVGNYDT 420
361 ISRLLPBSPDMVTLAIPDKLTWNTLYQIRAFPSGOBLANVQIBRENSKSTKVGNYDT 420
Qy 421 NSSVQDKFAYELSDQKREBLOQPIGAVDPLSDSVTFNDSCGESESSEHQPTDDH 480
421 NSSVQDKFAYELSDQKREBLOQPIGAVDPLSDSVTFNDSCGESESSEHQPTDDH 480
Db 480 LSKLQVYDQKREBLOQPIGAVDPLSDSVTFNDSCGESESSEHQPTDDH 480
QY 481 SPSTASPYCRTTSKSDTEPOQKQSQQSGRTSSDDPGTCNSTDSTOQVLLGKRLKAETL 540
481 SPSTASPYCRTTSKSDTEPOQKQSQQSGRTSSDDPGTCNSTDSTOQVLLGKRLKAETL 540
Db 541 ELSLDIVSKDKDMAPPIERETSDQKLTQDINGNLMEKLERKLNRSRBCRSRSPPIKK 600
541 ELSLDIVSKDKDMAPPIERETSDQKLTQDINGNLMEKLERKLNRSRBCRSRSPPIKK 600
Qy 601 TSLSPTKLGYSYSDLAQKHSRQPSDPAERTTIAHADHSKKVQHRLSRQ 660
601 TSLSPTKLGYSYSDLAQKHSRQPSDPAERTTIAHADHSKKVQHRLSRQ 660
Db 660 DLSLSPKLGYSYSDLAQKHSRQPSDPAERTTIAHADHSKKVQHRLSRQ 660
QY 661 ELSKERARVLLQARRODAALKAGNKENTNTTPCNCRQLSDQDERRQLRERAROLAE 720
661 ELSKERARVLLQARRODAALKAGNKENTNTTPCNCRQLSDQDERRQLRERAROLAE 720
Db 720 ARSGVNSLEPSYGENAAKERSKASGRDNIDTPTHEPIPGFVGGDELNLN 780
721 ARSGVNSLEPSYGENAAKERSKASGRDNIDTPTHEPIPGFVGGDELNLN 780
Db 780 DLDTPRQNSKVDLKLKGKJLVEQPQVANSISSAACKAVNTTTPCNCRQLSDQDERRQLRERAROL 840
781 DLDTPRQNSKVDLKLKGKJLVEQPQVANSISSAACKAVNTTTPCNCRQLSDQDERRQLRERAROL 840
Db 840 SQ Sequence 1231 AA;

QY 841 TTERFPNVVPSKOSTWRKQLOSSQTYIERNPEMKRQSTQDFTKGGNEKAATFQR 900
841 TTERFPNVVPSKOSTWRKQLOSSQTYIERNPEMKRQSTQDFTKGGNEKAATFQR 900
Db 901 KPSEDEVNLNGKFQDTSQVYVGLAALNEQKQIDTRALVERKRYLMDTGNTTBTEAM 960
901 KPSEDEVNLNGKFQDTSQVYVGLAALNEQKQIDTRALVERKRYLMDTGNTTBTEAM 960
QY 961 MOBWFMLVNLNKGNALIRRMMOLSLRERHDLFRRYSLNRSRAMIAEDHQTEQRRE 1020
961 MOBWFMLVNLNKGNALIRRMMOLSLRERHDLFRRYSLNRSRAMIAEDHQTEQRRE 1020
Db 1021 QLLDDBLVAVNLKDALVRLDAQEKOABEDEHLERTLEONKGMAKKEKCVLQ 1076
Db 1021 QLLDDBLVAVNLKDALVRLDAQEKOABEDEHLERTLEONKGMAKKEKCVLQ 1076
RESULT 3
ADX07701
ID ADX07701 standard; protein; 1231 AA.
XX
AC ADX07701;
XX
DT 21-APR-2005 (first entry)
XX
CYCLIN-DEPENDENT KINASE MODULATION BIOMARKER SEQ ID NO 2266.
XX
CYTOSTATIC: CYCLIN-DEPENDENT KINASE; CDK; BIOMARKER.
XX
OS Homo sapiens.
XX
FN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PP 29-JUL-2004; 2004WO-US024424.
XX
FR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR 2005-163068/17.
DR N-PDB; ADX07701.
XX
PT BIOMARKERS USEFUL FOR PREDICTING OR DETERMINING THE RESPONSE OF A MAMMAL TO A CANCER TREATMENT COMPRISING ADMINISTRATION OF A MODULATOR OF CYCLIN-DEPENDENT KINASE ACTIVITY.
XX
CLAIM 5; SEQ ID NO 2266; 141PP; English.
XX
This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 274 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-(5-(1,1-dimethylethyl)-2-oxazolyl)methyl]thio]-2-thiacyl-4-piperidine carboxamide, 0.5-L-tartric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ipo.int/pub/published_pct_sequences. This sequence represents a biomarker used in the method of the invention.

Query Match	99.2%	Score	5442.5	DB	9	length	1231	
Best Local Similarity	96.6%	Pred.	No. 0	; Mismatches	1			
Matches	1073	Conservative		Indels	2			
QY	1	MKQYASPMPTOTDVKLKFPLSKVVAALQFLSCLIFRLREGKATDEDMOSLASIVSMQ	60					
Db	121	MKQYASPMPTOTDVKLKFPLSKVVAALQFLSCLIFRLREGKATDEDMOSLASIVSMQ	60					
QY	61	AIDGNLDDFEDNEDDEENRWNQERAAKIT.....	91					
Db	181	ADGNLDDFEDNEDDEENRWNQERAAKIT.....	91					
QY	92	-----ELINKLNLTDEAKDLATNSNPFPDPDAEINPFGDDESEREPITETASPRKE	145					
Db	241	SASSBEBELINKNLTVEARAKDLATNSNPFPDPDAEINPFGDDESEREPITETASPRKE	145					
QY	146	DSFTNNSYMPFKEYTPTQYINPPDEPEARTVTKIUSPPOSTKRNIPVMYSKLYADSK	205					
Db	301	DSFTNNSYMPFKEYTPTQYINPPDEPEARTVTKIUSPPOSTKRNIPVMYSKLYADSK	205					
QY	205	TERHELDENSPPYRKSTPPNNUNPVQLETERRRVKKAPAPVLSKGTGVLENVENTS	265					
Db	361	TERHELDENSPPYRKSTPPNNUNPVQLETERRRVKKAPAPVLSKGTGVLENVENTS	265					
QY	266	AGKDLSTSCKPSPIPSVPGGRKPAWASQSLIWVCEVTKVIRGVKLTNTFTSWRGLSFA	325					
Db	421	AGKDLSTSCKPSPIPSVPGGRKPAWASQSLIWVCEVTKVIRGVKLTNTFTSWRGLSFA	325					
QY	325	ILHHFRPDLDYKSLNPODIKENKKAYDFGFASTGISRLIEPSDMVLLAIPDKLTWMTL	385					
Db	481	ILHHFRPDLDYKSLNPODIKENKKAYDFGFASTGISRLIEPSDMVLLAIPDKLTWMTL	385					
QY	386	YQTRAHFSGQBLNTVQIBERNSSKSTYKVNTETJNSSTQEKYAEASLDKREPELQO	445					
Db	541	YQTRAHFSGQBLNTVQIBERNSSKSTYKVNTETJNSSTQEKYAEASLDKREPELQO	445					
QY	446	ISGAVDPLSQDSDYFUNDSCVGESSESEHQTDDHLSPTASPKCRTKSDTEPKQSQSS	505					
Db	601	ISGAVDPLSQDSDYFUNDSCVGESSESEHQTDDHLSPTASPKCRTKSDTEPKQSQSS	505					
QY	505	GRISGSDDRGICCSNTDSTORAQVILGGKRLLKAETLBSLDLYVSDRKKKOMSPPFCTEETD	565					
Db	661	GRISGSDDRGICCSNTDSTORAQVILGGKRLLKAETLBSLDLYVSDRKKKOMSPPFCTEETD	565					
QY	566	QKLQTLDGTSNLNEGEKLENSRSUCLCRSDPESPIKTSISPTSKLGYSRSRDLAKKHA	625					
Db	721	QKLQTLDGTSNLNEGEKLENSRSUCLCRSDPESPIKTSISPTSKLGYSRSRDLAKKHA	625					
QY	626	SIROTESPDADRTLNHADHSSKVHRLSROELKERARVILLEQARDALKAGNH	685					
Db	781	SIROTESPDADRTLNHADHSSKVHRLSROELKERARVILLEQARDALKAGNH	685					
QY	686	NTNTATPFCNRQLSDQDQEERRRQLERARQLTAEARSCVWKMBLSPSYGEMAAKLRKS	745					
Db	841	NTNTATPFCNRQLSDQDQEERRRQLERARQLTAEARSCVWKMBLSPSYGEMAAKLRKS	745					
QY	746	KASGDENDNIEIDTNEPTEPEGFVGGDGLTLNLENDLTPEQNSKLUKLKULXEQPO	805					
Db	901	KASGDENDNIEIDTNEPTEPEGFVGGDGLTLNLENDLTPEQNSKLUKLKULXEQPO	805					
QY	806	VANSPSSAAQAKTETESSEODMKSTEDRTERLQKTTTERPRNPVVKSDSTVRKTQLOSP	865					
Db	961	VANSPSSAAQAKTETESSEODMKSTEDRTERLQKTTTERPRNPVVKSDSTVRKTQLOSP	865					
QY	866	SQTENRDEMFKRQSIQEDTKKGMEBKAIETTORKPSDEVLNGKGFDTQSIVGELAA	925					
Db	1021	SQTENRDEMFKRQSIQEDTKKGMEBKAIETTORKPSDEVLNGKGFDTQSIVGELAA	925					
QY	926	LENBOKOIDTRALVEKRLYLMGTGRNTEERAMMQWFMUMLKKNLIRNMOLSLIE	985					
Db	1081	LENBOKOIDTRALVEKRLYLMGTGRNTEERAMMQWFMUMLKKNLIRNMOLSLIE	985					
QY	1081	LENBOKOIDTRALVEKRLYLMGTGRNTEERAMMQWFMUMLKKNLIRNMOLSLIE	1140					
QY	986	KHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY	986	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
Db	1141	KEHDLERVELLNLRLMAISDWQKTAQRRLQDDELVALVNGRDALVRDQDQF	1045					
QY	1046	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
Db	1201	KQABEBDEBLERTEQNQKOMAKKEBCKUQ	1076					
QY</								

CC sclerosis, meningitis, brain abscess, prion disease, Creutzfeldt-Jakob
 CC disease, insomnia, neurofibromatosis, cerebral palsy, myasthenia gravis,
 CC anxiety. The present amino acid sequence represents a human SCAP of the
 CC invention.

SQ Sequence 1040 AA:

Query Match 95.9%; Score 5266; DB 7; Length 1040;
 Best Local Similarity 96.6%; Pred. No. 2.8e-316; Mismatches 0; Indels 36; Gaps 1;

Db Matches 1039; Conservative 1; Mismatches 0; Indels 36; Gaps 1;

QY 1 MKQYASPMPTQDVKUKPKPSKKVVAALQSLSCIPLRKGATDMDMQLASLVSMSQ 60
 1 MRQYASPMPTQDVKUKPKPSKKVVAALQSLSCIPLRKGATDMDMQLASLMSMQ 60
 1 AELNPFGDPSSPEPITETASRKTEDSPYNNSYNPFRKVQTYLNPPDBEAFVTKDS 120
 1 AELNPFGDPSSPEPITETASRKTEDSPYNNSYNPFRKVQTYLNPPDBEAFVTKDS 120
 1 ADIGNDDPFDNEDDENRQEENRQEAKATTELINKANPLDEBAKDLATVNPNPDPA 120
 1 ADIGNDDPFDNEDDENRQEENRQEAKATTELINKANPLDEBAKDLATVNPNPDPA 120
 121 AELNPFGDPSSPEPITETASRKTEDSPYNNSYNPFRKVQTYLNPPDBEAFVTKDS 180
 121 AELNPFGDPSSPEPITETASRKTEDSPYNNSYNPFRKVQTYLNPPDBEAFVTKDS 180
 181 PPOSTERKNITFVDMKYLMDSSKTEREBEDIDESNFYPPEPSTPPPNLYNPWOLETER 240
 181 PPOSTERKNITFVDMKYLMDSSKTEREBEDIDESNFYPPEPSTPPPNLYNPWOLETER 240
 241 RYVKRKAAPPPLSPKGVLNTVSAGKDLTSKPSPISSPVGPKPKPNAQSLLWCKE 300
 241 RYVKRKAAPPPLSPKGVLNTVSAGKDLTSKPSPISSPVGPKPKPNAQSLLWCKE 300
 301 VTKNYRGVKINTFTSWRNGISPCATLHHFRPDLDIYKSJNPQDIKENNKAYDGPASIG 360
 301 VTKNYRGVKINTFTSWRNGISPCATLHHFRPDLDIYKSJNPQDIKENNKAYDGPASIG 360
 361 ISRLLEIPSDMVLIAFDKLTVNTYLIQIRAMPSGOBLNVYQIEENNSKSTKVGNYETDT 420
 361 ISRLLEIPSDMVLIAFDKLTVNTYLIQIRAMPSGOBLNVYQIEENNSKSTKVGNYETDT 420
 421 NSSVQDEKFYELSDLQREPLQOPISGAVDPLQDSDSVFNDSGVGESSESHQPDH 480
 421 NSSVQDEKFYELSDLQREPLQOPISGAVDPLQDSDSVFNDSGVGESSESHQPDH 480
 421 NSSVQDEKFYELSDLQREPLQOPISGAVDPLQDSDSVFNDSGVGESSESHQPDH 480
 481 SPSTASPYCRTKSDEPQKQQSSGRTSQQDDPGICSNNTDSTQAVLGLGRKLIAETL 540
 481 SPSTASPYCRTKSDEPQKQQSSGRTSQQDDPGICSNNTDSTQAVLGLGRKLIAETL 540
 QY 541 ELSLDIVSKDKDMPPFICETBDQKLTQDLSNLKEKLNRSLRGSRSPIKK 600
 541 ELSLDIVSKDKDMPPFICETBDQKLTQDLSNLKEKLNRSLRGSRSPIKK 600
 601 TSLSPTKLGSYSRDLAKKKHSRLQTESPDADRTTINAHDSKQVHRLRSQE 660
 601 TSLSPTKLGSYSRDLAKKKHSRLQTESPDADRTTINAHDSKQVHRLRSQE 660
 661 ELSKERVILLEQARRODAALKGKRNNTATTPCURLQSLDQDEERRQLERASQIAE 720
 661 ELSKERVILLEQARRODAALKGKRNNTATTPCURLQSLDQDEERRQLERASQIAE 720
 QY 721 ARSGVMSLPSYGENMAEKERSKAGBENDNTIDTMRHEIPSGFWGGDELNLN 780
 721 ARSGVMSLPSYGENMAEKERSKAGBENDNTIDTMRHEIPSGFWGGDELNLN 780
 721 ARSGVMSLPSYGENMAEKERSKAGBENDNTIDTMRHEIPSGFWGGDELNLN 780
 Db 721 ARSGVMSLPSYGENMAEKERSKAGBENDNTIDTMRHEIPSGFWGGDELNLN 780
 Db 721 ARSGVMSLPSYGENMAEKERSKAGBENDNTIDTMRHEIPSGFWGGDELNLN 780
 781 DLDITPRQNSKUVDKLUKLUQPOVANSSISAQKAVTESRQMSKSCEDRTERLQ 840
 781 DLDITPRQNSKUVDKLUKLUQPOVANSSISAQKAVTESRQMSKSCEDRTERLQ 840
 750 - - - BONSKVLVDKLUKLUQPOVANSSISAQKAVTESRQMSKSCEDRTERLQ 804
 QY 841 TERFRNPVWFSKDSVTVKTQLOFSQYIERPEMKRQS1QEDTKGNKNEAKAETTOR 900
 QY 805 TTERFRNPVWFSKDSVTVKTQLOFSQYIERPEMKRQS1QEDTKGNKNEAKAETTOR 864
 QY 901 KPSDEBVNLKQKDTQSQQVYGLAALENKQDITRAVLYERLRLYMDTGNTTREBAM 960
 QY 925 MQEWFMVNLKNAITTRMNQLSLLEKHLRERYELLNLRLAMLAEDWQTKAQRR 984

Db 865 KPSDEBVNLKQKDTQSQQVYGLAALENKQDITRAVLYERLRLYMDTGNTTREBAM 924
 QY 961 MOBWFMLVNLKNAITTRMNQLSLLEKHLRERYELLNLRLAMLAEDWQTKAQRR 1020
 Db 925 MQEWFMVNLKNAITTRMNQLSLLEKHLRERYELLNLRLAMLAEDWQTKAQRR 984

Db 1021 QLILDSVALVNRDALVLDQSKAESDEHLERTLEONKGKMAKKEKCVLQ 1076
 Db 985 QLILDSVALVNRDALVLDQSKAESDEHLERTLEONKGKMAKKEKCVLQ 1040

R5ULT 5
 AM78788
 ID AAM78788 standard; protein; 1581 AA.
 XQ
 AC AAM78788;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1450.
 XX
 PR 03-FEB-2000; 2000US-00436914.
 PR 27-APR-2000; 2000US-00530875.
 PR 20-JUN-2000; 2000US-00538075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00634936.
 PR 15-SEP-2000; 2000US-00633561.
 PR 20-OCT-2000; 2000US-00633325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PD 09-AUG-2001.
 XX
 PP 05-FEB-2001; 2001WO-US004998.
 XX
 PR 03-FEB-2000; 2000US-00436914.
 PR 27-APR-2000; 2000US-00530875.
 PR 20-JUN-2000; 2000US-00538075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00634936.
 PR 15-SEP-2000; 2000US-00633561.
 PR 20-OCT-2000; 2000US-00633325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 (HYSB-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT, Abundi V, Zhou P, Xu C, Cao Y;
 BI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZN;
 PI Xue AJ, Yang Y, Wejhran T, Goodrich R;
 XX DR WPI: 2001-476283/51.
 DR N-PSDB; AAK51921.
 XX
 PR Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PR in diagnosis and gene therapy.
 XX
 PR Claim 20; Page 3716-3718; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haemopoiesis regulating
 activity, tissue growth factor activity, immunomodulatory activity and
 activin/inhibin activity and may be useful in the diagnosis and/or
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation. Note: Records for ID NO 2110 (AAK5581), 2111
 (AAK52582) and 3666 (AAW8020) are omitted as the relevant pages from the
 sequence listing were missing at the time of publication

SQ Sequence 1581 AA:

Query Match	94.4%; Score 5183; DB 4; Length 151;	Db	
best Local Similarity	67.6%; Conservative 1; Mismatches 1; Indels 512; Gaps 1;	Qy	
Matches 1068;		Qy	
b		Db	
8 MPTQTDVKLKEPLSKRVSALQFSLSCIFLREGKATDEDMQSLASLVMKQADIGNLD	67	1081 GAVDPLSQDDSVFVNDSGVGESEBHQTPDDHLSRSTASPCYRRTKSDEPQKQQSSR	1140
1 MPTQTDVKLKEPLSKRVSALQFSLSCIFLREGKATDEDMQSLASLVMKQADIGNLD	60	1000 -----	999
b		Qy	
68 DFEEDNEDDENVRNQEBEAKTIBELINKUNFLDEAKTDLATVNNSPFDDPAAEINPRG	127	1141 TSGSDPGICNTSISTQAQVLGKGRLLGATELFLSDVSKKDMSPPPICHTDEQK	1200
61 DPEEDNEDDENVRNQEBEAKTIBELINKUNFLDEAKTDLATVNNSPFDDPAAEINPRG	120	1000 -----	999
b		Qy	
128 DPDSEPIETASPKTEDESYNNSPKEVOTIYLNPFDEPAFTIKDQSPOSTER	187	1261 RQTSDDPADRTTLNHADHSKTVQHRLSRQELKERARVLEQARDAALKAGNKINT	1320
121 DPDSEPIETASPKTEDESYNNSPKEVOTIYLNPFDEPAFTIKDQSPOSTER	180	1201 LQTIDIGSNLEKEKLENSLECSDPESPIKITSLSPLTSKJ3SYSRDLDDAKKKHASL	1260
b		Qy	
188 KNIRPVDMSKLYADSSKTEBEELDENSPNPVEPKSTPPPNLNUVQELTERRYRKAP	247	1000 -----	999
Y		Db	
181 KNIRPVDMSKLYADSSKTEBEELDENSPNPVEPKSTPPPNLNUVQELTERRYRKAP	240	1261 RQTSDDPADRTTLNHADHSKTVQHRLSRQELKERARVLEQARDAALKAGNKINT	1320
b		Qy	
248 APPVLSPKTGIVLENNTSASKDLSTSPPKSPISPVPLGRKPNASOSLWACKVTKYRG	307	1000 -----	999
241 APPVLSPKTGIVLENNTSASKDLSTSPPKSPISPVPLGRKPNASOSLWACKVTKYRG	300	1381 SGEONSKVLDDKLKLEVOPQVANSPSSAAQAVTESSEBODMKGSTDRLTERLOKTE	1440
b		Qy	
308 VKITMFTTSWRNGISFCATLHFRDLIDKSLNQDKKENNKAYGFA SIGSRLSLP	367	1000 -----	999
301 VKITMFTTSWRNGISFCATLHFRDLIDKSLNQDKKENNKAYGFA SIGSRLSLP	360	1441 RFRIIPVWSKDSTRKTQLOFSFCYIENRPEMKQRSTQEDTKGNBKAITEIQKPS	1500
b		Qy	
368 SDMVLLAIPDKLTWMTLYQTRAHSGQEJNUVQETBENNSKSTYKVGNYNTDNSSDQ	427	1000 ---ELRAMIAELWOKTAQREBOLUDDELVALVNLKDADYRDLDAQBKABEDEHL	1055
421 KFYABLSDLKREPELQOPTSGAVDPLS QDDSVFVNDGVGESESEHOTPDDHLSRSTASP	480	1501 EDEVELRAMIAELWOKTAQREBOLUDDELVALVNLKDADYRDLDAQBKABEDEHL	1560
b		Qy	
488 YCRRKSTKSTERQKSCQSGCTGSDDPGICNSNTDSTAQVLGKRLKJAKTELSDLV	547	1056 ERTVQNKOKWAKREKCVLQ	1076
481 YCRRKSTKSTERQKSCQSGCTGSDDPGICNSNTDSTAQVLGKRLKJAKTELSDLV	540	1561 ERTVQNKOKWAKREKCVLQ	1581
b		Db	
548 SDKKKDDMSPPPICEETDEQKLQTIDIGSNLEKEKLENSLECSDPESPIKITSLSPTS	607	RESULT 6	
541 SDKKKDDMSPPPICEETDEQKLQTIDIGSNLEKEKLENSLECSDPESPIKITSLSPTS	600	AAM79773	
b		ID AAM79773 standard; protein; 1023 AA.	
608 KLGYSYSRDLDLACKKHASLROTESDDPADRTTLNHADHSKTVQHRLSRQELKERAR	667	AC	
601 KLGYSYSRDLDLACKKHASLROTESDDPADRTTLNHADHSKTVQHRLSRQELKERAR	660	XX	
b		DT 06-NOV-2001 (first entry)	
668 VLIQARRDALKAGNKHNNTAPFCNRQLSDQDERRQLRERARQLIAERSGTM	727	XX	
661 VLIQARRDALKAGNKHNNTAPFCNRQLSDQDERRQLRERARQLIAERSGTM	720	DR Human protein SEQ ID NO 3419.	
b		XX	
728 SELPSYGMEMAKJKRSKASGDDENDIRIDTNBEPPEGFVGCGDDELNLENDLDTPEQ	787	KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; hematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.	
721 SELPSYGMEMAKJKRSKASGDDENDIRIDTNBEPPEGFVGCGDDELNLENDLDTPEQ	780	XX	
b		OS Homo sapiens.	
788 NSKLVDLKLKLLLEVOPQVANSPPSAAKAVTESSEBODMKGSTDRLTERLOKTERPN	847	XX	
781 NSKLVDLKLKLLLEVOPQVANSPPSAAKAVTESSEBODMKGSTDRLTERLOKTERPN	840	PN WO20015190-A2.	
b		XX	
848 PWVSKDSTRKTQLOFSFCYIENRPEMKQRSTQEDTKGNBKAITEIQKPSDEV	907	PD 09-AUG-2001.	
b		XX	
841 PWVSKDSTRKTQLOFSFCYIENRPEMKQRSTQEDTKGNBKAITEIQKPSDEV	900	PP 05-FEB-2001; 2001WO-US004098.	
b		XX	
908 LNKGPFRDTSQYVVBELALENEQOIDTRALVERKRLVMDTGRNTTERBAMOBWFM	967	PR 03-FEB-2000; 2000US-00496914.	
b		PR 27-APR-2000; 2000US-00560875.	
901 LNKGPFRDTSQYVVBELALENEQOIDTRALVERKRLVMDTGRNTTERBAMOBWFM	960	PR 20-JUN-2000; 2000US-00598075.	
b		PR 19-JUL-2000; 2000US-00620325.	
968 VNKKNALIRRNQQLSLKEHDLLERYELNR-----	999	PR 01-SEP-2000; 2000US-00654936.	
b		PR 15-SEP-2000; 2000US-00663561.	
961 VNKKNALIRRNQQLSLKEHDLLERYELNRGJSRLBSDMVLLAIPDKLTWMTLYQ	1020	PR 20-OCT-2000; 2000US-00693325.	
b		PR 30-NOV-2000; 2000US-00728422.	
b		XX	
1000 -----		PA (HYSB-) HYSECO INC.	

XK Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; PI Ma Y, Zhao QA, Wang D, Wang J, Ren F, Chen R, Wang ZW; PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XK DR WPI; 2001-47283/51.
XK N-PSDB; AAK52906.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

XK Claim 20; Page 328-329; 6221pp; English.

CC CC The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW8322-AAW0302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and/or polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52501), 2111 (AAK52502) and 3666 (AAW0020) are omitted as the relevant Pages from the sequence listing were missing at the time of publication

CC CC (AAK52582)

CC CC sequence listing were missing at the time of publication

XX SQ Sequence 1023 AA;

Query Match Best Local Similarity 94.2%; Score 5173; DB 4; Length 1023; Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0; QY 63 IGNLDPEEDHEDDENRWNQBEKAKITBLINKNPKLNPLDELEKQDLATVNNSPPDDPAE 122 Db 10 LANLDPFEDHEDDENRWNQBEKAKITBLINKNPKLNPLDELEKQDLATVNNSPPDDPAE 69 QY 123 IAPFGDPDSEPRITETASPRITEDSFYNNISNPKEVQTYQQLNPFDEPEAFVTIKDSP 182 Db 70 LNPFGDPDSEPRITETASPRITEDSFYNNISNPKEVQTYQQLNPFDEPEAFVTIKDSP 129 QY 183 OSTKRKNIRTPDMSKTYLAISSKTREBBLRSNPFPKSTTPPNLUNPVQELTERV 242 Db 130 OSTKRKNIRTPDMSKTYLAISSKTREBBLRSNPFPKSTTPPNLUNPVQELTERV 189 QY 243 KRKAPELLSPKPGVLANENTVSAGDLSPSKPPIPSPVTLGRIENASQSLWCKEV 302 Db 190 KRKAPELLSPKPGVLANENTVSAGDLSPSKPPIPSPVTLGRIENASQSLWCKEV 249 QY 303 KNYRGKIKMTFTSWRNLGSFCAILHHFRPDLLDYKLSNFQDKIENKKKGADGFAIGIS 362 Db 250 KNYRGKIKMTFTSWRNLGSFCAILHHFRPDLLDYKLSNFQDKIENKKKGADGFAIGIS 309 QY 363 RLLERPSDMVLLAIPDKLTWVMTYOLRAHFSQGBQJNQVQETNSKSTYKVNEYDTNS 422 Db 310 RLLERPSDMVLLAIPDKLTWVMTYOLRAHFSQGBQJNQVQETNSKSTYKVNEYDTNS 369 Qy 423 SVDOQKPYARSLDKEPELQPIGAVIDPSQDSSVYFNDGCVGESESEHQTPDHLS 482 Db 370 SVDOQKPYARSLDKEPELQPIGAVIDPSQDSSVYFNDGCVGESESEHQTPDHLS 429 QY 483 STASPYCRRTSDTEOKSQOSSGRTSGSDPGICNTSSTAQVNLIGKRLKQETL 542 Db 430 STASPYCRRTSDTEOKSQOSSGRTSGSDPGICNTSSTAQVNLIGKRLKQETL 489 QY 543 SDLYVSDKKKMSPPCICERDEOKLQTLIGSNLREKLRNSRLECRSDPESPIKTS 602 Db 490 SDLYVSDKKKMSPPCICERDEOKLQTLIGSNLREKLRNSRLECRSDPESPIKTS 549 Qy 603 LSPTSKLGYSISRDIDLAKKHASIQTESPDAIRTTLHADISKIVQRHLRSQEE 662 Db 550 LSPTSKLGYSISRDIDLAKKHASIQTESPDAIRTTLHADISKIVQRHLRSQEE 609

Query Match Best Local Similarity 94.2%; Score 5173; DB 4; Length 1023; Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0; QY 663 KERRAVILLEQARDAAKAGKHNNTATPCNRQLSDQODBERRQLRERQRLTAA 722 Db 610 KERARVILQARRDAAKAGKHNNTATPCNRQLSDQODBERRQLRERQRLTAA 669 QY 723 SGVKMSELPSGYEMAELKERSKASGDDENNTIDTNESEPEGFVGGDPELTNLNDL 782 Db 670 SGVKMSELPSGYEMAELKERSKASGDDENNTIDTNEE1PEGFVGGDPELTNLNDL 729 QY 783 DTPEONSKLVQKLKLUKLYQPOVANSPPSSAAQAVTESRQDMGSGTEDRTERQKT 842 Db 730 DTPEONSKLVQKLKLUKLYQPOVANSPPSSAAQAVTESRQDMGSGTEDRTERQKT 789

Db 843 ERPRINVURSKDSTRKTOLOFSQYIENPEMKQRSIQEDTKGNERKAITETQRKP 902
Db 790 ERPRINVURSKDSTRKTOLOFSQYIENPEMKQRSIQEDTKGNERKAITETQRKP 849

QY 903 SDEBVAKNGFKDTSQVVGELAALENEQKQDTRAAVEKRLYAMDGRNTEERBAMMQ 962
Db 850 SDEBVAKNGFKDTSQVVGELAALENEQKQDTRAAVEKRLYAMDGRNTEERBAMMQ 909

QY 963 EWFMVLNKQKALIREMNQLSLKEHDLLERYELNRLPAMTALEDWQTEACKRERQL 1022
Db 910 EWFMVLNKQKALIREMNQLSLKEHDLLERYELNRLPAMTALEDWQTEACKRERQL 969

QY 1023 LLDBLVALVNGRDLAQKQAEEDHELTBLQNGKROMAKKREKCVLQ 1076
Db 970 LLDBLVALVNGRDLAQKQAEEDHELTBLQNGKROMAKKREKCVLQ 1023

RESULT 7
AM7772
ID AAM7772 standard; protein; 1023 AA.
AC AAM7772;
XX DT 06-NOV-2001 (first entry)
XX Human protein SEQ ID NO 3418.
DB Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory activity; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
KW Homo sapiens.
OS OS
FN W0200157190-A2.
XX PD 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US004098.
XX 03-FEB-2000; 2000US-00496914.
PR 27-PR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00520325.
PR 01-SEP-2000; 2000US-0054935.
PR 15-SEP-2000; 2000US-00653561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSB-) HYSBQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX DR WPI; 2001-47283/51.
XX N-PSDB; AAK52905.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

PS Claim 20; Page 328; 6221pp; English.

xx CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AMW823-AMW80302) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haemopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activity/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: Records for SEQ ID NO 2110 (AAK5381), 2111
(AMW8020) and 3666 (AMW8020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

xx SQ Sequence 1023 AA;

Query Match

Best Local Similarity 94.2%; Score 5173; DB 4; Length 1023;

Matches 1011; Conservative 99.7%; Fred. No. 1.6e-310; Mismatches 2; Bases 1023; Indels 0; Gaps 0;

QY 63 IGNLDDEEEDNEDDENRINQEBEAKAKITELINKUNFLDEAKOLATVNNSPFDPPDAAS 122
Db 10 LANIDDPREINEDDENRINQEBEAKAKITELINKUNFLDEAKOLATVNNSPFDPPDAAS 69
QY 123 LNPFGDDPDSEBEPITETASPRKTEPSFYNNSYNPKEVQTPQYLNPFDEPAFVTKDSSP 182
Db 70 LNPFQGDPDSEBEPITETASPRKTEPSFYNNSYNPKEVQTPQYLNPFDEPAFVTKDSSP 129
QY 183 QSTKRKNTRPVDMSKYLYADSKTTEERELDESNPYERPKSTPPPNLYVPQELETERV 242
Db 130 QSTKRKNTRPVDMSKYLYADSKTTEERELDESNPYERPKSTPPPNLYVPQELETERV 189
QY 243 KRKAPELLSPKTOVLNTVSAGKDLSTPKCSPIPSPVPLGKPNASQSLIWCKEWT 302
Db 190 KRKAPELLSPKTOVLNTVSAGKDLSTPKCSPIPSPVPLGKPNASQSLIWCKEWT 249
QY 303 KNYRGVKITNTTSWRNGLSPFCATLAHFRFDLIDYKSINPDIKENNKAYDGASIGTS 362
Db 250 KNYRGVKITNTTSWRNGLSPFCALIHFRFDLIDYKSINPDIKENNKAYDGASIGS 309
QY 363 RLLRSPDMVLLAIPDKLTMTLYQIRAHFSQELNVQIEENSNSKSTYKVGNYETDMS 422
Db 310 RLLRSPDMVLLAIPDKLTMTLYQIRAHFSQELNVQIEENSNSKSTYKVGNYETDMS 369
QY 423 SDORKFVYELSDJKREPLQQLQPSGAVDPLSQDSDVFNDSGYGESESERQPDHDHSP 482
Db 370 SDQEKFVYELSDJKREPLQQLQPSGAVDPLSQDSDVFNDSGYGESESERQPDHDHSP 429
QY 483 STASPYCRAFTKSDTEPKQSQQSSRTSGSDDPGICSNNTDSTQAOVLLGKCRRLKAETBL 542
Db 430 STASPYCRAFTKSDTEPKQSQQSSRTSGSDDPGICSNNTDSTQAOVLLGKCRRLKAETBL 489
QY 543 SLDYVSKCKDMSPPFICRTEBDQKLQTLIGSNEKELENSRSRSPPIKTS 602
Db 490 SLDYVSKCKDMSPPFICRTEBDQKLQTLIGSNEKELENSRSCLCRSPPIKTS 549
QY 603 LSPTSKLGYSYSRSDLALLKKHASLRQTESPDADRTLNHADHSKIVQHRLSQRBL 662
Db 550 LSPTSKLGYSYSRSDLALLKKHASLRQTESPDADRTLNHADHSKIVQHRLSQRBL 609
QY 663 KERARVILLEQARRDAALKAGNKHNTATPPCNQOLSDQDDEERRQRLRERAROLIAZAR 722
Db 610 KERARVILLEQARRDAALKAGNKHNTATPPCNQOLSDQDDEERRQRLRERAROLIAZAR 669
QY 723 SGVNRSEPSYGENMAKEKERSKASGDENDFIDTNEIPIRGFVWGGDLSNLNDL 782
Db 670 SGVNRSEPSYGENMAKEKERSKASGDENDFIDTNEIPIRGFVWGGDLSNLNDL 729
QY 783 DTPEQNSKLVLKLUKJLKFVQPOVANSSESAQGVATSESSQDMKGSRDLRERLOKTT 842
Db 730 DTPEQNSKLVLKLUKJLKFVQPOVANSSESAQGVATSESSQDMKGSRDLRERLOKTT 789

QY 843 ERFRNPVVFSDSTRKTKOLOQSQYIENRPEMKQRSIQDTKGNBEEAATETQRKP 902
Db 790 ERFNPVVFSDSTRKTKOLOQSQYIENRPEMKQRSIQDTKGNBEEAATETQRKP 849
QY 903 SEDESTLKKGKDTSQYVYGBLALENKQDIDTRALTYEKRLYLMDTGCRNTBEBAMHQ 962
Db 850 SEDEVNLKGKDTSQYVYGBLALENKQDIDTRALTYEKRLYLMDTGCRNTBEBAMHQ 909
QY 963 EWFMLVNUKNAIRRNMQSLRBRKEDLERYELLNRSLRAMIAEDMKTQKRRQL 1222
Db 910 EWFMLVNUKNAIRRNMQSLRBRKEDLERYELLNRSLRAMIAEDMKTQKRRQL 969
QY 1023 LLDELVALVNUKDALVRLDQAQEKAESDEHBLTLCNGKMAKCEKCVLQ 1076
Db 970 LLDSLVALVNUKDALVRLDQAQEKAESDEHBLTLCNGKMAKCEKCVLQ 1023

RESULT 8

ABG22883 standard; protein; 1023 AA.

XX

AC ABG22883;

XX

DT 18-FEB-2002 (first entry)

XX

DB Novel human diagnostic protein #22874.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200115067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

XX

23-AUG-2000; 2000US-00649167.

XX

PA (HYSB-) HYSEQ INC.

XX

PT Dumanac RT, Liu C, Tang YN;

XX

DR WPI; 2001-639362/73.

XX

N-PSDB; AAS81070.

XX

PS Claim 20; SEQ ID NO 53242; 103pp; English.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX

PS

Claim 20; SEQ ID NO 53242; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridization probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight marker and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide Sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG03077 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences
XX

Db	910	BWFLVLVNGNALLRMQQLSLLKEHDLLRYELLNLRLMLAEDWQKTAQKRREQL	969
QY	1-023	LIDDELVALVNKDALVALDIDAEKQEEDEDEHLERLTERLEONKGKMKRKEBCVLO	1-076
D _b	970	LIDDELVALVNKDALVALDIDAEKQEEDEDEHLERLTERLEONKGKMKRKEBCVLO	1-023

CC composition and method are useful for treating a disease or disorder,
 CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
 CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
 CC autoimmune disorders, viral infection, or cancer. This is the amino acid
 sequence of a novel polypeptide of the invention.

SQ Sequence 1023 AA;

Query Match 93.9%; Score 5152; DB 9; Length 1023;
 Best Local Similarity 99.3%; Pred. No. 3.1e-309; Matches 1007; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy : |||||GNTLDPFEDNEDDENRVMQWEEKAKEITELINKNPLDEBKDLATVNSNPDDPDAE 122
 Db 10 LANLDDPFEDNEDDENRVMQWEEKAKEITELINKNPLDEBKDLATVNSNPDDPDAE 69
 Qy 123 LNPFGDPDSEPRITETASPRITEDSFYNNSYNPKEVQTPQYLNIPDEPAPFTIKDPP 182
 Db 70 LNPGDPDSEPRITETASPRITEDSFYNNSYNPKEVQTPQYLNIPDEPAPFTIKDPP 129
 Qy 183 OSTKRENIRPDMSKYLYADSSKTERBEBEDSNPFPKSTPPNLTUNVQELTERRY 242
 Db 130 OSTKRENIRPDMSKYLYADSSKTERBEBEDSNPFPKSTPPNLTUNVQELTERRY 189
 Qy 243 KRKAPPAPPVLSKPGVLANENTVSACKLSTSRSKOSPIPSVULGRKPNASQSLWCKEV 302
 Db 190 KRKAPPAPPVLSKPGVLANENTVSACKLSTSRSKOSPIPSVULGRKPNASQSLWCKEV 249
 Qy 303 KNYRGKIKNTFTSWSNGLSSFCALIJKHFRDLDIYKSINQDIDKENNKAYDGASIGIS 362
 Db 250 KNYRGKIKNTFTSWSNGLSSFCALIJKHFRDLDIYKSINQDIDKENNKAYDGASIGIS 309
 Qy 363 RLLERPSDMVIAIIPDKLTWMTYQIRAHSGQBLNVOBENNSKTYKGNTETDMS 422
 Db 370 SVDOBKPYAISLSDLKREPELQOPTSGAVDPLSPQDSPPVFDNSGVGRSESHQTPDHLSP 429
 Qy 310 RLLERPSDMVIAIIPDKLTWMTYQIRAHSGQBLNVOBENNSKTYKGNTETDMS 369
 Qy 423 SVDQKPYAISLSDLKREPELQOPTSGAVDPLSPQDSPPVFDNSGVGRSESHQTPDHLSP 482
 Db 430 STASPYCRRIKSDTRPKQSQQSGRTSGSDPGICNTSITQAQLIGKERRKARTEL 542
 Qy 543 SDLVYSDDKKKWDMSPPICBETDEQKLQTLDGSNLKEKLNSRLCRRDDESPIKITS 602
 Db 490 SDLYVSDDKKWDMSPPICBETDEQKLQTLDGSNLKEKLNSRLCRRDDESPIKITS 549
 Qy 603 LSPTRSKLGYSYSDLDLAKCHASLRQTSDDPDRDTIHAHDSSKTIYHRILSRQEL 662
 Db 550 LSPTRSKLGYSYSDLDLAKCHASLRQTSDDPDRDTIHAHDSSKTIYHRILSRQEL 609
 Qy 663 KERARVILLEQARRDAAKAGKHNNTATPFCNRQSLDQODBERQRRLRQARLAEAR 722
 Db 610 KERARVILLEQARRDAAKAGKHNNTAFCNRQSLDQODBERQRRLRQARLAEAR 669
 Qy 723 SGVKMSELPSYGEMAKBLKURSKASGDENDNIRDTNEIPEGFWGAGDNLNL 782
 Db 670 SGGMKMSLPSYGERAKBLKURSKASGDENDNIRDTNEIPEGFWGAGDNLNL 729
 Qy 783 DTPGONSKLVLQDALKLLEYQPVANSPPSAQAKVTESSRQDMKSGTEDLIRTLQKT 842
 Db 730 DTPBONSKLVLQDALKLLEYQPVQANSPSSAQAKVTESSBQDMKSGTEDLIRTLQKT 789
 Qy 843 BRFRNPVWVSKDSTRKTOQFSQVIENTPEMKRQSQBDTKGNBKAETORKP 902
 Db 790 ERFRPFWVSKDSTRKTOQFSQVIENTPEMKRQSQBDTKGNBKAETORKP 849
 Qy 903 SEDDEVLINKGKGDTSQYVGRALALENEQKOIDTRALVEKLRVMDTNTTERRAMNO 962
 Db 850 SEDDEVLINKGKGDTSQYVGRALALENEQKOIDTRALVEKLRVMDTNTTERRAMNO 909
 Qy 963 EWFMLVNUKQVALIRRNQQLSULEKEHDLERYELLNRKLMATEDWQXTEAQKRREGQI 1022

RESULT 11
 ARA21082
 ID AEA21082 standard; protein; 1023 AA.
 AC ARA21082;
 XX DT 11-AUG-2005 (first entry)
 XX Novel human polypeptide SEQ ID NO 1776.
 XX
 KW vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
 KW DNA purification; protein purification; osteoarthritis; antiarthritic;
 KW osteopatric; musculoskeletal disease; osteoporosis; endocrine disease;
 KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
 KW peripheral neuropathy; Alzheimer's disease; neuroprotective; nontropic;
 KW degeneration; parkinsons disease; anti-parkinsonian; neurological disease;
 KW cerebrovascular ischemia; cerebroprotective; vasotropic;
 KW cardiovascular disease; autoimmune disease; immunosuppressive;
 KW immune disorder; viral infection; virucide; infection; cancer;
 KW cytostatic; neoplasm.
 XX
 OS Homo sapiens.
 XX
 WO2005049806-A2.
 PN
 XX
 PD 02-JUN-2005.
 XX
 PR 11-MAR-2004; 20044NO-US007412.
 XX
 PA (NUVUE) NUVELO INC.
 XX
 PI Tang YY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
 PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
 PI Weinman T, Weng G, Boyle B;
 XX
 DR WPI; 2005-4177304/2.
 XX
 PT New polynucleotide encoding a polypeptide with biological activity
 PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
 PT CNS and peripheral disease, stroke, autoimmune disorders, viral
 PT infection, or cancer.
 XX
 PS Example 3; SEQ ID NO 1776; 500pp; English.

The invention describes a new isolated polynucleotide (1) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes to the sequence of (1) under stringent hybridization conditions; or a nucleotide sequence having greater than 99% sequence identity with the sequence of (1). Also described are: a(n) (expression) vector comprising (1), a host cell genetically engineered to comprise (1) operatively, the associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide (1) is a polypeptide encoded by (1); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3); a method for detecting (1) in a sample; a method for detecting the polypeptide of (3) in a sample; a method for identifying a compound that binds to the polypeptide of (3); a method of producing the polypeptide of (3); and a collection of polynucleotides, where the collection comprising of at least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of

the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined within the specification. The sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or other traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and amino acid sequences. These composition and method are useful for treating a disease or disorder, e.g., osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This is the amino acid sequence of a novel polypeptide of the invention.

Db	790	ERFRIPVVFVKOSTTRKTQLOPSQTENRPEMKQRQSIOETKGNBKAITETORQ	849
Qy	903	SEDEVINKGKDTSOTWVGELAALNEQKQDTRAALVEKURLYMGTGRNTEERAMHQ	962
Db	850	SEDEVINKGKFDSQYVUGELAALNEBOKQIDTRAALVEKURLYMGTGRNTEEBAMHQ	909
Qy	963	EWPMJUVNKQALIRRMNQLSLEKENDLERYELLABRLAMLAISWQKEBAQRREQL	1022
Db	910	EWPMJUVNKQALIRRMNQLSLEKENDLERYELLABRLAMLAISWQKTAQKRRLQ	969
Qy	1023	LLDSEVALVNKRDALVRDLOQEKAEEDDEHLRTLEQONKGKMAKCEBCKYLQ	1076
Db	970	LLDDELVALVNKRDALVRDLOQEKAEEDDEHLRTLEQONKGKMAKKREKCVLQ	1023

CC polynucleotide hybridizing under stringent conditions with any one of SEQ
 CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
 CC carrier; an antibody directed against the polypeptide of (3); a method
 CC for detecting (1) in a sample; a method for detecting the polypeptide of
 CC (3) in a sample; a method for identifying a compound that binds to the
 CC polypeptide of (3); a method of producing the polypeptide of (3); and a
 collection of polynucleotides, where the collection comprising of at
 least one of SEQ ID NOS: 1-567; (1) is a polynucleotide comprising any of
 the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
 activity, which comprises any of the amino acid sequence of SEQ ID NOS:
 568-1134. All sequences are fully defined in the specification. The
 sequences and methods are useful in diagnostics, forensic, and gene
 mapping, in identifying mutations responsible for genetic disorders or
 other traits, in assessing biodiversity, and for producing many other
 types of data and products dependent on DNA and amino acid sequences. The
 composition and method are useful for treating a disease or disorder,
 e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
 peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
 autoimmune disorders, viral infection, or cancer. This is the amino acid
 sequence of a novel polypeptide of the invention.

Sequence 996 AA;

Query Match 91.8%; Score 5037; DB 9; Length 996;
 Best Local Similarity 99.4%; Pred. No. 3.8e-302; Matches 986; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 85 RAKAAKTEILINKUNFLDEAEDLTLATNSNPDDPDAEALRPGDPDSEPERITETASPRK 144

Db 5 RSASSEBLINLNFLDEAEDLTLATNSNPDDPDAEALRPGDPDSEPERITETASPRK 64

Qy 145 EDSFINNNSYNPKVEVQTPQIAPPDAEPAFTIKOSPPQSTKRKNIRPVDMSKYJADSS 204

Db 65 EDSFINNNSYNPKVEVQTPQIAPPDAEPAFTIKOSPPQSTKRKNIRPVDMSKYJADSS 124

Qy 205 KTEEBELDESHNPYFVKRSTPPNNLYNPVQDLERTERVRKIAAPPLVSLPRTGIVAMENTV 264

Db 125 KTEEBELDESHNPYFVKRSTPPNNLYNPVQDLERTERVRKIAAPPLVSLPRTGIVAMENTV 184

Qy 265 SAGKDLSTSPPSPPTPSVPGCRKPNAQSILWMCCKTUVKTRGRVKLTNFTPSWRGLSFC 324

Db 185 SAGKDLSTSPPSPPTPSVPGCRKPNAQSILWMCCKTUVKTRGRVKLTNFTPSWRGLSRC 244

Qy 325 ALHHRFPDLIDYKSLANPODKKENNKAYDGPASIGISRLKPSDMLVLAIPDKLKVMTY 384

Db 245 ALHHRFPDLIDYKSLANPODKKENNKAYDGPASIGISRLKPSDMLVLAIPDKLKVMTY 304

Qy 385 LYQIRAHFSGCBLNVYQIBENSKSKTYKVGETTNTNSSYDQEKTYAELSDKLRBPELOO 444

Db 305 LYQIRAHFSGCBLNVYQIBENSKSKTYKVGETTNTNSSYDQEKTYAELSDKLRBPELOQ 364

Qy 445 PISGAVDLSQDSDYEVNDGGVGEBSERSEKHTPDHLSRSPASPCRTTSDETEROKSQS 504

Db 365 PISGAVDLSQDSDYEVNDGGVGEBSERSEHOPDHLSPSPASPCRTTSDETEROKSQS 424

Qy 505 SGRTSGSDDPQICSNSTDQVQLIGKKRKAETELSLDIYVSDKRDQKMSPPFCETD 564

Db 425 SGRTSGSDDPQICSNSTDQVQLIGKKRKAETELSLDIYVSDKRDQKMSPPFCETD 484

Qy 565 EOKLQTDIGSNLEKEKLNSLRSCLRSRSPKTKTSLSPTSKLGYSYRDLAKKKH 624

Db 485 EOKLQTDIGSNLEKEKLNSLRSCLRSRSPKTKTSLSPTSKLGYSYRDLAKKKH 544

Qy 625 ASLRTQESPDADRTTINHADHSSKLVORHLSRDELKERARVILQARDAAKAGNK 684

Db 545 ASLRTQESPDADRTTINHADHSSKLVORHLSRDELKERARVILQARDAAKAGNK 604

Qy 685 HNTNTATPPCIRQLSDQQDBERRQRARQLIARSGKMSLPSKCEMAEKKER 744

Db 605 HNTNTATPPCIRQLSDQQDBERRQRARQLIARSGKMSLPSKCEMAEKKER 664

Qy 745 SKASGDENDNTEDTNEBIRPFGVWEGGDELTNLENDDTBQNKSQVLDLKKLLEVQP 804

RESULT 13

AAM39322

ID AAM39322 standard; protein; 996 AA.

AC AAM39322;

XX

DT 22-OCT-2001 (first entry)

XX

DB Human polypeptide SEQ ID NO 2467.

XX

KW Human; notropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoractic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

FD 26-JUL-2001.

XX

FP 26-DEC-2000; 2000WO-US034263.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-0058942.

PR 19-JUL-2000; 2000US-0060312.

PR 03-AUG-2000; 2000US-0053450.

PR 14-SEP-2000; 2000US-0062191.

PR 19-OCT-2000; 2000US-00633036.

PR 29-NOV-2000; 2000US-00727344.

XX

(HYSEQ) HYSEQ INC.

XX

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX

DR WPI; 2001-442253/47.

DR N-P3DB; AAI58478.

XX

Novel nucleic acids and polypeptides, useful for treating disorders such

as central nervous system injuries.

XX

Example 4; SEQ ID NO 2467; 1007pp; English.

XX

The invention relates to human nucleic acids (AAI57798-AAI61369) and the

Db 665 SKASGDENDNTEDTNEBIRPFGVWEGGDELTNLENDDTBQNKSQVLDLKKLLEVQP 724

Qy 805 QVANSPSAQAQAVTESBQDMKSCPTEDLTERLOXTRPFRNPFVFSKOSTVRKIQLOQS 864

Db 725 QVANSPSAQAQAVTESBQDMKSCPTEDLTERLOXTRPFRNPFVFSKOSTVRKIQLOQS 784

Qy 865 FSQYENRPENPMKROSIQERTTKGSMEKAITEORKPSSEDEVINKGKUTSOTVNGELA 924

Db 785 FSQYENRPENPMKROSIQBTJKGKHEKAALITEORKPSSEDEVINKGKUTSOTVNGELA 844

Qy 925 ALLENBKQIDTRAALVERKRLYLMGTGRNTEBEAMQEMFMLVANKNALLRMMOLSL 984

Db 845 ALLENBKQIDTRAALVERKRLYLMGTGRNTEBEAMQEMFMLVANKNALLRMMOLSL 904

Qy 985 EKEHDLERRYELLNLBRMLAIEDWQTEAQKREBQOLLDELVALVNKRKDVALVRDIDAQ 1044

Db 905 EKEHDLERRYELLNLBRMLAIEDWQTEAQKREBQOLLDELVALVNKRKDVALVRDIDAQ 964

Qy 1045 EKQABEDEHLLERTLEBQNKQKMAKEKCYVQ 1076

Db 965 EKQABEDEHLLERTLEBQNKQKMAKEKCYVQ 996

CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
 CC is: a polypeptide encoded by (1); or a polypeptide encoded by a
 CC polynucleotide hybridizing under stringent conditions with any one of SEQ
 CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
 carrier; an antibody directed against the polypeptide of (3); a method
 for detecting (1) in a sample; a method for detecting the polypeptide of
 (3) in a sample; a method for identifying a compound that binds to the
 polypeptide of (3); a method of producing the polypeptide of (3); and a
 collection of polynucleotides where the collection comprising of at
 least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of
 the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
 activity, which comprises any of the amino acid sequences of SEQ ID NOS:
 568-1134. All sequences are fully defined in the specification. The
 sequences and methods are useful in diagnostics, forensic, and gene
 mapping, in identifying mutations, for genetic disorders or
 other traits, in assessing biodiversity, and for producing many other
 types of data and products dependent on DNA and amino acid sequences. The
 composition and method are useful for treating a disease or disorder,
 e.g., osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
 peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
 autoimmune disorders, viral infection, or cancer. This is the amino acid
 sequence of a novel polypeptide of the invention.

SQ Sequence 960 AA:

Query Match 87.8%; Score 4817; DB 9; Length 960;

Best Local Similarity 95.8%; Pred. No. 1. 4e-288; Matches 950; Conservative 2; Mismatches 4; Indels 36; Gaps 1; Qy 85 EKAKAKITELINKLNFLDEBKAQDLATNSNPDDPAEQLNPRGDPDSESPRTETASPRK 144 Db 5 RSASSSSELINKLNFLDEBKAQDLATNSNPDDPAEQLNPRGDPDSESPRTETASPRK 64 Qy 145 EDSFVANSYNNPKEVQTPOQINPDPBARTIKOSPPQSTKRKRIRPVDMISKYADSS 204 Db 65 EDSFVANSYNNPKEVQTPOQINPDPBARTIKOSPPQSTKRKRIRPVDMISKYADSS 124 Qy 205 KTEEEBLDESDNPFPYERKSTPPDPNLNVPGDLETERVKRKAAPPVPLSPKGVLNTV 264 Db 125 KTEEEBLDESDNPFPYERKSTPPDPNLNVPGDLETERVKRKAAPPVPLSPKGVLNTV 184 Qy 265 SAGKDLSTSPPSPSPSPSPVLRGKPNASQSLIUVCKEVTKYRGKVNFTTSWRNGLSFC 324 Db 185 SAGKDLSTSPPSPSPSPVLRGKPNASQSLIUVCKEVTKYRGKVNFTTSWRNGLSFC 244 Qy 325 AILHHRPDLYDKISLNQDITKENKAYDOPASIGISRLPEPSMLLAPDQLTUMTY 384 Db 245 AILHHRPDLYDKISLNQDITKENKAYDOPASIGISRLPEPSMLLAPDQLTUMTY 304 Qy 385 IYQIRAHFSGOELNVVQIEENSSKSTKVGMVETDNTNSVDOEQKFVAFSLDKREPELOQ 444 Db 305 LYQIRAHFSGOELNVVQIEENSSKSTKVGMVETDNTNSVDOEQKFVAFSLDKREPELOQ 364 Qy 445 PISGAVDPLSDODSVTFNDSCVGESISBSHOPDDHHSUPSPASPYCRRTKSIDTEROKSQQ 504 Db 365 PISGAVDPLSDODSVTFNDSCVGESISBSHOPDDHHSUPSPASPYCRRTKSIDTEROKSQQ 424 Qy 505 SGRTSSDDPPICSWNSTDQTVLGLKRLJAKTELSDIVSKKKKOMSPPFCESTD 564 Db 425 SGRTSSDDPPICSWNSTDQTVLGLKRLJAKTELSDIVSKKKKOMSPPFCESTD 484 Qy 565 EQLQTDIGENLEKEKLENSRSLECRSPPIKTSLSPTSKUGYSYRDLDLAKKH 624 Db 485 EQLQTDIGENLEKEKLENSRSLECRSPPIKTSLSPTSKUGYSYRDLDLAKKH 544 Qy 625 ASLROTESDPADRTLNHMHSSKLVORHLSRQEKLKRRARVILQARDAALKAGNK 684 Db 545 ASLROTESDPADRTLNHMHSSKLVORHLSRQEKLKRRARVILQARDAALKAGNK 604 Qy 685 HINTNTATPFCRQLSQQDERRQRLERARQLIAERSGWMSLPSKGEMAAKLER 744 Db 605 HINTNTATPFCRQLSQQDERRQRLERARQLIAERSGWMSLPSKGEMAAKLER 664

Qy 745 SKASGDENDNIEKDITNBIFPFGVVGGDSLTLNLENDTPRQNSKVLVDJKLKKLURVQP 804 Db 665 SKASG-----EONSKLVDIKLKQLEVQP 688 Qy 805 QWANSPSSAQAQAVTESSEQDMKSGTEDLDRLOKTTFRNPVPUFSKOSTVRKTOLOS 864 Db 689 QWANSPSSAQAQAVTESSEQDMKSGTEDLDRLOKTTFRNPVPUFSKOSTVRKTOLOS 748 Qy 865 FSOYIERNPEMKRQSIQBETTKGKHEKAATETORKPSDEVLNGKFKTSQYVQGELA 924 Db 749 FSOYIERNPEMKRQSIQBETTKGKHEKAATETORKPSDEVLNGKFKTSQYVQGELA 808 Qy 925 ALENEQKQDITRAALVERKURYMDTGTRNTBAMMOWFPMUWKKKALIRRMOUL 984 Db 809 ALENEQKQDITRAALVERKURYMDTGTRNTBAMMOWFPMUWKKKALIRRMOUL 868 Qy 985 EKEDLIRRVEYLNLNEBLRAMLAEDWQKTEAQKQRZBQLLDBLVALVNRKDALVRLDAQ 1044 Db 869 EKEDLIRRVEYLNLNEBLRAMLAEDWQKTEAQKQRZBQLLDBLVALVNRKDALVRLDAQ 928 Qy 1045 EKOABEBDEHLERTLHQNKWKAKCERKCVLQ 1076 Db 929 EKOABEBDEHLERTLHQNKWKAKCERKCVLQ 960

RESULT 15
 ADJ70136
 ID ADJ70136 standard; protein; 882 AA.
 XX
 AC ADJ70136;
 XX
 DT 06-MAY-2004 (first entry)
 DB Human heat mitochondrial protein as a therapeutic target
 SeqID1942.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis; LION;
 KW Leber's hereditary optic neuropathy; MION;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERFF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteoprotective; ophthalmological; cryostatic;
 KW ophthalmic;
 OS Homo sapiens.
 XX
 WO2003087768 A2.
 XX
 WO2003087768 A2.
 XX
 PDD 23-OCT-2003.
 XX
 FP 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0312843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 PA
 PI Gosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DR;
 XX
 WPI: 2003-845369/7B.

Identifying a mitochondrial target for drug screening assays and for
 treating diseases associated with altered mitochondrial function,
 comprising detecting a modified polypeptide in a sample and correlating
 with the disease.

Claim 1; SEQ ID NO 1942; 180pp; English.
 This invention relates to novel mitochondrial targets that can be used
 for therapeutic intervention in treating a disease associated with an
 altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are used for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such targets that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytoprotective activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

XX
SQ Sequence 882 AA:

Query Match 81.7%; Score 4485; DB 7; Length 882;
Best Local Similarity 100.0%; Pred. No. 4e-268; Matches 882; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 MISKLYADSSRTEEELDSESNPPFPKSTPPNNTVPNPVQBLERERRVKRKAPAPPVSP 254
Db 1 MISKLIVYADSSRTEEELDSESNPPFPKSTPPNNTVPNPVQBLERERRVKRKAPAPPVSP 60
QY 255 KTGIVLAVENTWAGKOLSTSPPKSPRSPVPLGKRNKAQSOLIVWCKEVTKVTRGKIKTFT 314
Db 61 KTGIVLAVENTWAGKOLSTSPPKSPRSPVPLGKRNKAQSOLIVWCKEVTKVTRGKIKTFT 120
QY 315 TSWNLGLSFCAILHHRPDLIYKSLNRPDKKENKKAYDGASIGISRLRSMDVLLA 374
Db 121 TSWNLGLSFCAILHHRPDLIYKSLNRPDKKENKKAYDGASIGISRLRSMDVLLA 180
QY 375 IPDKLUTVMTYLYQIRAHFSGQELNVQIRENSSIKYKVGNEYDTNSVDOBKPYAEL 434
Db 181 IPDGLUTVMTYLYQIRAHFSGQELNVQIRENSSIKYKVGNEYDTNSVDOBKPYAEL 240
QY 435 DLKRREPPELQQPIGAQDFPSQDDSVFVNDSGGGESSEHOTPDHLSRSTAASPCCRRTS 494
Db 241 DLKRREPPELQQPIGAQDFPSQDDSVFVNDSGGGESSEHOTPDHLSRSTAASPCCRRTS 300
Qy 495 DTBPKQSOSSGRSGSDPGICNTSDQAQVLGKRLKATLTLSDLYSDKKDM 554
Db 301 DTBPKQSOSSGRSGSDPGICNTSDQAQVLGKRLKATLTLSDLYSDKKDM 360
Db 555 SPPPCICEEDBKQLQTDIGSLRKEKLENSRLCERSDPESPIKTSISPTSKLGYS 614
Db 361 SPPPCICEEDBKQLQTDIGSLRKEKLENSRLCERSDPESPIKTSISPTSKLGYS 420
Qy 615 RDIDLAKKKGHSALKQTESPDADRTLNHADHSSKIVORHLSSLRERLKERARVILBOAR 674
Db 421 RDIDLAKKKGHSALKQTESPDADRTLNHADHSSKIVORHLSSLRERLKERARVILBOAR 480
Qy 675 RDAALKAGSKHNTATPFCNROISDQDDEERRRERLBARQLTAANGGVNSELPSYG 734
Db 481 RDAALKAGSKHNTATPFCNROISDQDDEERRRERLBARQLTAANGGVNSELPSYG 540
Qy 735 EMMAEKLKERSKASGDENDIEIDTNEETPFGVNGGDELNLENDIDTPEGNSKLVDL 794
Db 541 EMMAEKLKERSKASGDENDIEIDTNEETPFGVNGGDELNLENDIDTPEGNSKLVDL 600
Qy 795 KKLKULLEVQPOVANSPSSAQAKVTESSQDMKSGTEDLRTLRQLKTTERFRNPFVFSKD 854
Db 601 KUKKULLEVQPOVANSPSSAQAKVTESSQDMKSGTEDLRTLRQLKTTERFRNPFVFSKD 660
Qy 855 STVRKTKQLOSPSOYTIENREMMKRSIQTDTKGKNEKAITELORKSSEDEVJNKGKD 914
Db 661 STVRKTKQLOSPSOYTIENREMMKRSIQTDTKGKNEKAITELORKSSEDEVJNKGKD 720
Qy 915 TSQYNGELLALENENQKQDTRALVEKRLYLMGTGRNTEERAMMQEWFFMLVJKQAL 974
Db 721 TSQYNGELLALENENQKQDTRALVEKRLYLMGTGRNTEERAMMQEWFFMLVJKQAL 780
Qy 975 IRRNQNLISLKEHDLRLRYELARELRLMAMLAEDWQKTEAKRERQEQLILDELVALKR 1034

Db 781 IRRNQNLISLKEHDLRLRYELARELRLMAMLAEDWQKTEAKRERQEQLILDELVALKR 840
Qy 1035 DALVRDLDQKQKREBEERBLERLTLEQKQKMKKRESCVYLQ 1076
Db 841 DALVRDLDQKQKREBEERBLERLTLEQKQKMKKRESCVYLQ 882

Search completed: May 20, 2006, 17:09:12
Job time : 207 secs

FEATURE: ;
NAME/KEY: misc_feature
LOCATION: (0).-(0)
OTHER INFORMATION: Polypeptide Accession Number P46939
US-09-538-092-1136

Query Match 5.9%; Score 326.5; DB 2; Length 3433;
Best Local Similarity 19.8%; Prec. No. 216-12; Mismatches 336; Index 303; Gaps 37;
Matches 197; Conservative 159; MisMatches 336; Indels 303; Gaps 37;

QY |||||||ISRLIEPDSMVLIAIPDKLTVMVYKQIRAHPSQELNVOIENSSKSTYKVNEDT 420
361 ISRLIEPDSMVLIAIPDKLTVMVYKQIRAHPSQELNVOIENSSKSTYKVNEDT 420
361 ISRLIEPDSMVLIAIPDKLTVMVYKQIRAHPSQELNVOIENSSKSTYKVNEDT 420

QY |||||||NSVDQEKYAESDLKREPELQPIGSAVDFSQODDSFVNDSGGGBSEHQTPDHL 480
421 NSVDQEKYAESDLKREPELQPIGSAVDFSQODDSFVNDSGGGBSEHQTPDHL 480
421 NSVDQEKYAESDLKREPELQPIGSAVDFSQODDSFVNDSGGGBSEHQTPDHL 480

QY |||||||SPSTASPYCRRTKSDEPORKSOQSRSRGSQSDPGICCSNTSDAQAVLGKMLKAETL 540
481 SPSTASPYCRRTKSDEPORKSOQSRSRGSQSDPGICCSNTSDAQAVLGKMLKAETL 540
481 SPSTASPYCRRTKSDEPORKSOQSRSRGSQSDPGICCSNTSDAQAVLGKMLKAETL 540

QY |||||||RSLDLYVSKDKKOMSPPICRETDQKLOTLDSGSNUKEJLNSLECRSPSPPIKK 600
541 RSLDLYVSKDKKOMSPPICRETDQKLOTLDSGSNUKEJLNSLECRSPSPPIKK 600
541 RSLDLYVSKDKKOMSPPICRETDQKLOTLDSGSNUKEJLNSLECRSPSPPIKK 600

QY |||||||TSLSPTSKLGSISRDLAKKHHASLROTESPDADRTLNHADASSKIVORLLRQE 660
601 TSLSPTSKLGSISRDLAKKHHASLROTESPDADRTLNHADASSKIVORLLRQE 660
601 TSLSPTSKLGSISRDLAKKHHASLROTESPDADRTLNHADASSKIVORLLRQE 660

QY |||||||ELCKERARVILLEQARRDAALKAGKHNNTATPPCNRQLSDQDQBERRQLRQE 720
661 ELCKERARVILLEQARRDAALKAGKHNNTATPPCNRQLSDQDQBERRQLRQE 720
661 ELCKERARVILLEQARRDAALKAGKHNNTATPPCNRQLSDQDQBERRQLRQE 720

QY |||||||ARSGVKOSBLSPLSGMAEKLKRSKASGDENDNIEIDTNELIPFGFNGGGDELNLN 780
721 ARSGVKOSBLSPLSGMAEKLKRSKASGDENDNIEIDTNELIPFGFNGGGDELNLN 780
721 ARSGVKOSBLSPLSGMAEKLKRSKASGDENDNIEIDTNELIPFGFNGGGDELNLN 780

QY |||||||DLDTPPEQNSKLVDLKKLKLVEPOVANSPSSAAQKAVTESSQDMSGTEDLRERLQK 840
781 DLDTPPEQNSKLVDLKKLKLVEPOVANSPSSAAQKAVTESSQDMSGTEDLRERLQK 840
781 DLDTPPEQNSKLVDLKKLKLVEPOVANSPSSAAQKAVTESSQDMSGTEDLRERLQK 840

QY |||||||TTERPRNIVPSKSTDVTKTOLQSFQSYTIENRPMKRSICQDTKGKNEKTAITEQR 900
841 TTERPRNIVPSKSTDVTKTOLQSFQSYTIENRPMKRSICQDTKGKNEKTAITEQR 900
841 TTERPRNIVPSKSTDVTKTOLQSFQSYTIENRPMKRSICQDTKGKNEKTAITEQR 900

QY |||||||KSEDEBEVJNKGFQDTSTQVNGELALEBNOKDTRALVALVEKRLYLMDTGRNTEEBAM 960
901 KSEDEBEVJNKGFQDTSTQVNGELALEBNOKDTRALVALVEKRLYLMDTGRNTEEBAM 960
901 KSEDEBEVJNKGFQDTSTQVNGELALEBNOKDTRALVALVEKRLYLMDTGRNTEEBAM 960

QY |||||||WQRMFLYNNKONALLRNMQLSLIKENDLERYLLEBLRMLAEDWQKTEAKRRE 1020
961 WQRMFLYNNKONALLRNMQLSLIKENDLERYLLEBLRMLAEDWQKTEAKRRE 1020
961 WQRMFLYNNKONALLRNMQLSLIKENDLERYLLEBLRMLAEDWQKTEAKRRE 1020

QY |||||||QILDEBLVALNRDLDQEKQREBEDHLERLTERLQNGKMKACEKCVLQ 1076
1021 QILDEBLVALNRDLDQEKQREBEDHLERLTERLQNGKMKACEKCVLQ 1076
1021 QILDEBLVALNRDLDQEKQREBEDHLERLTERLQNGKMKACEKCVLQ 1076

RESULT 2
US-09-538-092-1136
; Sequence 1136, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Iaic
; APPLICANT: Mansfield, Traci A.
; TITLE OR INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIORITY NUMBER: 60/127,352
; PRIORITY FILING DATE: 1999-04-01
; PRIORITY NUMBER: 60/178,965
; PRIORITY FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1136
; LENGTH: 3433
; TYPE: PRT
; ORGANISM: Homo sapiens

QY US-09-949-016-10918

Db 1024 DSTVIKEKMDGVDFPLNKQQAQGDAGLQRQLDQ 1058

RESULT 3

Sequence 10918 Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949, 016

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 10918

LENGTH: 2141

TYPE: PRT

ORGANISM: Human

US-09-949-016-10918

Query Match 5.5%; Score 307.5; DB 2; Length 2141;

Best Local Similarity 20.0%; Pred. No. 2, 4e-11; Matches 196; Conservative 165; Mismatches 318; Indels 303; Gaps 45;

QY 285 GRKP-NASQSLVWCKEVTKNTRGVKTNTFTSWRNGLSFCATLHHRPDLIDYKSANPQ 343

Db 173 GEETRSKADALIJCWQMTAGYPHWNTNFNTSSWKGQALFNLHHRPDLIDYKQD 232

Qy 344 DTKENKKAYD-GFASIGISRLSPSMVLAIPDKLTWMTLYQRAHFSQELNQVQI 402

Db 233 NARHNLEHAFNVAERQGILPILDED-PVTENPDEKSIITYVVAHYES--KMYTLAV 289

Qy 403 ENSKSKTYKVGMETINNSDQEKVTAHSLSL----- 436

Db 290 B---GRKVQKVIDHAETKMI---EKYQGLASDLMIWIEQTIVTIVMSRKANSLTQVQQ 344

Qy 437 -----KRPPELQOPTISGAVDPLSODDSVVFNUVGVERSESSESHOTPDHLSPTAS 486

Db 345 LQAFSTKRTVEKPKQS-KMNLVL---LFTPSMRMANNOKVTPHD--GKLV 394

Qy 487 PYCRRTMSDTEPKQSQQSGRTSGSDPORGICNSNTDQAQVULGKGRKLKATELSDSL 545

Db 395 DINRHWESLERABYRIR-----LALRHBLIGRBLQBLARR 430

Qy 546 YVSDEKKDMSPPFICE-----ETO-----BQLQTL-DI 573

Db 431 F---DRKAQMREWLSEMQVRLQDNYCFLANVEAKKKHBAETTAAVERVRALELD 488

Qy 574 GSNTLEKKEKLNSRSLCERSDPSPPIKTSLSPTSLSKGSYSRDLDDAKKKHSLRQTESD 633

Db 489 AQELEKRYVHDKRITARKONILRL-----WSYLQ---ELIQSRQRQLETTAL 534

Qy 634 PDADETRLNADHSSKIVQHRL-----LRQEELKJERAKVLEQARDALKAGKHN 686

Db 535 QKLPQDMHLHSIDWMDIEKAKHLLSABRGKHLLVEEDLQHKHM---EADIAIQ-GDKVK 589

Qy 687 INTATPP-----CNRQL-----SDQOQEB-----RQDQREARQL----- 717

Db 590 ATTAATUKTFEGKQYQCPDPQVTDISHLLOCPCERLSNMAGRKQI-EQSKRKLKFPW 648

Qy 718 -TAEANGVQKNSLPSGEMAEK-----LKERKASGDDENDNTEIDTMERIPE--GP 767

: ||| | : | : | : | : | : | : | : | : | : | : | :

Db 759 LIKWLQD-----AHLISGEDVQDGEGATRALGKHHKFLE---ELRSRGVMEHL 806

Qy 886 KKGNEBKAAITETORKPSEDETVLNKCFKDTSCQYVGEALALENEQKOIDTALEVKRL 945

Db 807 EQ-----QAQGFPEE-----FRD-SPDVTHRLQALRELKVQVVAQADLQRQL 849

Qy 946 YMDTGTGRANTEEEBAMQOBWFLVNKGNALTRRMNQSLISLKEHDLERRYELNRELRLAML 1005

Db 850 EALDLYVFGEDA-CBLW---MGEKEKMLAEMEPDTELEDLYVQHRFDQEMKTM 905

Qy 1006 AIED-----MO---KTEAQKRRQL----- 1022

Db 906 TQIDGWNLAAANSLVSNECHSPRSRBEVKYQDHINTRWQAFOQTIVSERKEAVDSALRVHNVYC 965

Qy 1023 -----LLB-----LVALVNTEDALYRD-----LDAQEKOAE- 1050

Db 966 DCBETSKWITDRTKVVESTKQDGLRDLAGITAIQKULGSLRSRQVAIQARYDALERESQL 1025

Qy 1051 EDEHLERTLBEQNGKOMAKKEK 1072

Db 1026 MDSHPHQ---KEDIGQRQKHLB 1045

RESULT 4

US-09-091-501B-10

Sequence 10, Application US/09091501B

GENERAL INFORMATION:

APPLICANT: Tinsley, Jonathon M

TITLE OF INVENTION: Urokinase gene expression

FILE REFERENCE: 620-42

CURRENT APPLICATION NUMBER: US/09/091, 501B

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: PCT/GB96/03156

PRIOR FILING DATE: 1996-12-19

PRIOR APPLICATION NUMBER: GB 9525962.8

PRIOR FILING DATE: 1995-12-19

PRIOR APPLICATION NUMBER: GB 9615797.9

PRIOR FILING DATE: 1996-07-26

PRIOR APPLICATION NUMBER: GB 9622174.2

PRIOR FILING DATE: 1996-10-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 10

LENGTH: 3433

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: NAME/KEY: misc_feature

LOCATION: (239) ... (250)

OTHER INFORMATION: Description of Artificial Sequence: Full length

OTHER INFORMATION: utrophin construct; Xaa = unknown

US-09-091-501B-10

Query Match 5.5%; Score 301.5; DB 2; Length 3433;

Best Local Similarity 19.6%; Pred. No. 1, 1e-10; Matches 190; Conservative 165; Mismatches 363; Indels 251; Gaps 36;

Qy 286 RPKNASQSLVWCKEVTKNTRGVKTNTFTSWRNGLSFCATLHHRPDLIDYKSANPQD 345

Db 148 QCTNSRKILLSWRQTRPVTSQVNLFNTSWTDGLAFNAVLHHRPKDPSWDRVVKMSP 207

Qy 346 KENNKKAYD-GFASIGISRLSPSMV-----LAIPIKLT-----VM 382

FILE REFERENCE: 59.US2.REG
 CURRENT APPLICATION NUMBER: US/09/513,999C
 PRIORITY FILING DATE: 2000-02-24
 PRIORITY APPLICATION NUMBER: US 60/122,487
 NUMBER OF SEQ ID NOS: 3681
 SOFTWARE: Patent.pn
 SEQ ID NO: 7173
 LENGTH: 61
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 16
 OTHER INFORMATION: Xaa=Ile or Lys or Arg or Thr
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 17
 OTHER INFORMATION: Xaa=Asp or Glu
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 39
 OTHER INFORMATION: Xaa=Asp or Glu
 US-09-513-999C-7173
 Query Match 5.4%; Score 296; DB 2; Length 61;
 Best Local Similarity 95.1%; Pred. No. 1; e-12; 0; Gaps 0;
 Matches 58; Conservative 0; Mismatches 3; Indels 0;
 Db 727 MSRLPSYCEMAAKLKKERSKASGDDENIDEIDNEEIPFEGFVGGGIBLTNLENDLDPTE 786
 1 MSELPLPSYCEMAAKLXXXSKASGDDENDIEIDNEEIPXGFVVGGSDELTNLENDLDPTE 60
 Qy 787 Q 787
 Db 61 Q 61

RESULT 6
 US-08-841-349-4
 Sequence 4, Application US/08841349B
 ; Paten No. 5955594
 ; GENERAL INFORMATION:
 ; APPLICANT: MISRA, LOPA
 ; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT...
 ; FILE REFERENCE: XX/PO4470US0
 ; CURRENT APPLICATION NUMBER: US/08/841,349B
 ; CURRENT FILING DATE: 1997-04-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 4
 ; LENGTH: 2154
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-08-841-349-4
 Query Match 5.3%; Score 291.5; DB 1; Length 2154;
 Best Local Similarity 20.3%; Pred. No. 2.8e-10; Mismatches 326; Indels 291; Gaps 38;
 Matches 194; Conservative 146; Mismatches 326; Indels 291; Gaps 38;
 Qy 287 KEPASQSLWCKRKEVTKYRGKIKNTTSRNGLSFCALWHRFDLIDKSLNPQDIK 346
 Db 159 KESAKDADLILWCOKMTAGPYNNINHFTTSWRDGMAFNALIKHRFDLIDKLGKSNAH 218
 Qy 347 ENKKKAND-GFASIGSLLEPSDMVLLAIKDLTWTMITYQIRAHFGQSBLAVVQ--- 401
 Db 219 YNLQNAAFLAEQHGLGLTMDPBD-1SDHPDKESITVVVYVHFSSKMLAVEGSKI 277
 Qy 402 --TEENSSKSTKVKVGNYET-----DTNSV 424
 Db 278 GKVLDNAIETKMIKETTLASDLLEWEIQTIIILNNRKFPANSLVGVQQQLQAFNTYRTV 337
 ; Patent No. 6793961
 ; GENERAL INFORMATION:
 ; APPLICANT: DUMAS Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6793961

RESULT 5
 US-09-513-999C-7173
 ; Sequence 7173, Application US/09513999C
 ; Patient No. 6793961
 ; GENERAL INFORMATION:
 ; APPLICANT: DUMAS Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6793961

Query Match 5.3%; Score 291.5; DB 2; Length 2154;
 Best Local Similarity 20.3%; Pred. No. 2.8e-10; Matches 194; Conservative 146; Mismatches 326; Indels 291; Gaps 38; Mismatches : 194; Conservative : 146; Mismatches 326; Indels 291; Gaps 38;

Db 338 EKPKPKTEKGNLLEVLFALPATOISKMRANNOVYMPRECKLISDINKAWERLER----- 388
 Qy 465 GVGEBSESHQPPDHSPSTASPICRTKSFTBPKSQSSGR----TSGSDPGICS 518
 Db 389 --AEERELALRNELIROEKELQBLAARFDRKRAMETWLSNQRJQSODNGFDPDAVEA 446
 Qy 519 NTDSQA-----OVLGKCRKLAKT----- 542
 Db 447 ATKKHEAETIAAYSERVOAVAVARBLEENHYDKRITARKDNVIRLWEYLBLRA 506
 Qy 543 -----SLVYSDKKDMSPPICE-----TDOKLOLTDIGS 575
 Db 507 RRQRLLEMNLGLQKIFQEMLYIMWDMDMKVLLSQDYGHILGVEDLQKHALVEADAI 566
 Qy 576 NLEKEKLENSSLESCKSDPE--SPIKTSI-SPTSKLGYSYSRDLDAKKHHSIQT-- 630
 Db 567 QASRVRGYNASAQEPAFATDGYKPCPQVDRVARMEFCYQELCOLAABRARIESRR 626
 Db 631 -----ESPDADRTLNHADHSKIVQ-HRLSLR---OBELKERARVILEQAR 674
 Db 627 LWKFPWEMAREBEGWIRKEKEKILSSDDYKGDTISVRLSKHRKFEDEMSGSG-HFEOAI 685
 Qy 675 RDAALKAGNKINTDATPFCNRQLSDQBERRQRLRERQRLAEARSTKMSLPSVG 734
 Db 686 KEGEDMIAEEH-----FGSEBKIRRTYIRBOWANL--BOSAIRKCRLEE-- 729
 Db 735 EMAEKKERSKASGDENDNIEIDTNEBIPGFVVGGD-----BLTNL 778
 Qy 730 ---ASLHQFOAADDDIAWMNDIKIVSNVD--GHDYSTOSLUVKKHWDVBLINC 783
 Db 779 ENDLPT-PEONSKLVULKLUKLEVPOV-ANSSSSAAQAVTESSEBQDMGSGTEDRTRB 836
 Qy 784 RPTDITLHEQASAL-----POAHAEPSDVKGRLAGIEERCKEMABLTR-LRKQ 830
 Qy 837 RLOKTERFRNPVUFVKSDTRKTOLQFSQYENRPEMKRQRSIQEPTKGNEKAIT 895
 Db 831 ALQDTIALYK---MFS-----BADACELWIDEKQWLNINMOP----- 866
 Db 897 STORKPSEDEVLNKGFKTSQVYVGBLAALNEOKOIDTRAALVEKRLYIMDGRTNBR 956
 Qy 867 ---KLEDLTIQHFR-----SLEPMENNQASRVAVNQIAROLMHCHPSEK 911
 Db 957 EAMMOB---WF---MLVNKGALIRRNMNQSLLEKEHDLRREYELLNLREMLMAI 1007
 Db 912 BIRAOQDKUNTRWSQFRELVDRKDAL--LISALSI-----QNTILBCNETKSCIR- 959
 Qy 1008 EDWOKTEAKRERQERQULLD--ELVALVNKRDAVLQDQE-----KOAB-EDEH 1054
 Db 960 ---EKTKVIESTODLGNDLAGVMALQCKLTOMERDVLVAIEAKLSDLQKEAKLESEH 1013
 RESULT 7
 US-09-431-184A-4.
 Sequence 4, Application US/09431184A
 ; Patent No. 6642362
 ; GENERAL INFORMATION:
 ; APPLICANT: MISHRA, LOPA
 ; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
 ; CURRENT APPLICATION NUMBER: US/09/431,184A
 ; CURRENT FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US98/08656
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: US 08/841,349
 ; PRIOR FILING DATE: 1997-04-30
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 2154
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-431-184A-4
 RESULT 8
 US-09-536-092-1243
 ; Sequence 1243, Application US/09538092

Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Giot, Loic
 APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 CURRENT APPLICATION NUMBER: US/09/538,092
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CurapatSeqFormatter Version 0.9
 SEQ ID NO: 1243
 LENGTH: 2364
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Polypeptide Accession Number Q01082
 US-09-538-092-1243

Query Match 5.3%; Score 289.5; DB 2; Length 2364;
 Best Local Similarity 19.3%; Pred. No. 4.2e-10;
 Matches 208; Conservative 171; Mismatches 369; Indels 331; Gaps 43;

QY 287 KPNASQSLUWCKEVTKMYRGVKTINFTSWRNGLSPCAILHHRPDLIDYSKSLNPQDTK 346
 Db 172 KKSADKALLWICMKTAGYPNVNINFTSWRNGLSPCAILHHRPDLIDYSKSLNPQDTK 346
 QY 347 ENNKAYD-GFASIGISRLPEPSDMVLAIPDKLTUMTYLYQIRAHFSQELNVQ--- 401
 Db 232 YNLQNAFNLAEQHLGLTLDPE-LSVDPHDPEKSITTVVTVTHYFSKOMKALAVEGRI 290
 QY 402 -IERNSSSKSTYKVGYET-----DTNSAV 424
 Db 291 GKVLNDNAITEKMTKYESLASDLEWIEBOTITLNRKFAFANSLVGVQQQLQAFNTYTV 350
 QY 425 DQEKEYAELSDLK-----RBEPELOOPIGSAVDELSQDDSVFVND 464
 Db 351 EKPKPRTEKGNLLEVLTIQSKMFRANNQKVTMPREGKLSDINTKAWERJEK----- 401
 QY 465 GVGSESEHOTPDHLSPLSTASPVCRTKSDTEPOKSOSGR----TGSDDPGICS 518
 Db 402 -AHEERELARNLIRQSKLEQLLARRFRDKAAKMRBTWILSENORLVSQDNFGFDLPAVEA 459
 QY 519 NTDSQA-----QVLUQSKRKAET-----LEL--- 542
 Db 460 ATKGHEAISTDIAAYEERVOAVAVARELAENHDIRKTRAKDNVIRLWWYELLEIRA 519
 QY 543 -----SDIVYSDKKKOMPPIPCB-----TDEQKQTDIGS 575
 Db 520 RQRLEMNLGQKIFOEMLYMDWDEMKTIVUSQDGKHLLSGYEDLIQKHTVYEADIGI 579
 QY 576 NEGEKLEMSRSLRCSRSDRE-SPIKTSI-SPTSKLGJYSRSRDLDAKKEKHSRLQT-- 630
 Db 580 QAERVGVVWASAQKREATDSRGKFCDPVIRDRVAMEMCYQELCQAAERRABLESRR 639
 QY 631 -----ESPDADRTLNHADHSKTVQ-HRLUSR---QEBLKARVLSBQR 674
 Db 640 LWKPFWMEMABEGWIREKEKSLSSDYGKFCDPVIRDRVAMEMCYQELCQAAERRABLESRR 698
 QY 675 RDALKAGKHK---NTNTATPCCRQLS--DQDEBRRLRERA-RQLEARS-- 723
 Db 699 KEGBDMAEEHFGSBKIRRIYIREQWANLEQSAIRKRLERASLHQFOADADDIDA 758
 QY 724 -----GVMSLPSYGEAMAUKERSKASGDENDNIE-IDTNEB---IPB---- 765
 Db 759 WMLQIKVSSDWGHDYESTQSLSVKHDDVAEETANTPTDOLTHEQASALQFEHASSP 818
 QY 766 --GFVVGGD-----ELTNL-----NDLDTP 785

RESULT 9
 US-09-635-795A-2
 Sequence 2, Application US/09/635-795A
 Patent No. 6808893
 GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 APPLICANT: ROHSTEIN, JEFFREY D.
 APPLICANT: JACKSON, Mandy
 APPLICANT: LIN, Glen
 APPLICANT: LAN, Robert
 APPLICANT: ORLOV, Irina
 TITLE OF INVENTION: GLUTAMATE TRANSPORTER ASSOCIATED PROTEINS AND METHODS OF USE THEREOF
 FILE REFERENCE: JH1650-2
 CURRENT APPLICATION NUMBER: US/09/695,795A
 CURRENT FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: US 60/161,007
 PRIOR FILING DATE: 1999-10-23
 PRIOR FILING DATE: 2000-05-22
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 2388
 TYPE: PRT
 ORGANISM: Rattus
 US-09-695-795A-2

Query Match 5.2%; Score 286; DB 2; Length 2388;
 Best Local Similarity 22.0%; Pred. No. 7.3e-10;
 Matches 200; Conservative 143; Mismatches 320; Indels 246; Gaps 41;

QY 287 KPNASQSLUWCKEVTKMYRGVKTINFTSWRNGLSPCAILHHRPDLIDYSKSLNPQDTK 346
 Db 175 KKSADKALLWICMKTAGYPNVNINFTSWRNGLSPCAILHHRPDLIDYSKSLNPQDTK 346
 QY 347 ENNKAYD-GFASIGISRLPEPSDMVLAIPDKLTUMTYLYQIRAHFSQELNVQ--- 405
 Db 235 YNLQNAFNLAEQHLGLTLDPE-VNDQDPEKSITTVVTVTHYFSKOMKALAVEGRI 289
 QY 406 SSKTKYKVNEDTNSQDQEKEYAELSKRPELQOPIGSAVDELSQDDSVFVND 465
 Db 290 -GRKGIVLHDHMEAHLV--EKYESLSEL-----LOWBOTIGTF-NDRQ 332
 QY 466 VGSESEHOTPDHLSPLSTASPVCRTKSDTEPOKSOSGRSGSGSDPGICNTSDTQA 525

Db 333 LANS-----LSGVQNQLQSPNSRT--VEKPP--KFTEKGNL 365
 Qy 526 QYLL-----GKCRLLKAETBLISLIVSDKKDMSPPPICRETDECKLTDIGS 575
 Db 366 EIVLFLPTIOSKURANNOVYTRREGRLISDINKAWERLEKA----EHEBIALRT---E 416
 Qy 576 NLERKCLENSESLECSDPSSPIKITSLSPTSKUGSYSRUDILAK----KXHASLRQT 630
 Db 417 LIRQFKEB--OLAARFDKAMREBTWLSENORLVSQDNIGGLEAVAEVURKHEI-ET 472
 Qy 631 ESDPDADRTTINAHADHSKIVOH----RLJSROB----LKB----RARVIL--- 670
 Db 473 DIVAVSGRVQDAVAAELAHEHYDIIKRIARONVARLMDPLKEMWAARRERLINLNE 532
 Qy 671 -----EQAQRDAALKAGKNHNTN- 688
 Db 533 LQKVFDQLLYINDDMMAEMKGRLQSODLGKHLAGVEDLQLHELVENDIAVQEVRAVA 592
 Qy 689 TATPPCN----RQLSDQOBER--RQLRERARQLIAERASGYOMSE---LPSYGE 735
 Db 593 SARFCDPGKEYRPGCPOLYVERSATEDSVEALCBLAATRARIRESRULWELWEVG 652
 Qy 736 MAABKLKERSKASGBENDNIBIDTNBIEPECGFVUGGDELNLNLEND----TPEONSK 790
 Db 653 ARAWTRREQQHMLASET----GRDITGVRLINKHTALRGEMSGR 693
 Qy 791 LVDLKLKLUFVEPOVANSPSSAAOKAVTESSE-ODMKSGSTEDLTERTLCQTTFRNPV 849
 Db 694 LGPLKL--TLHQGQOLVAEGHGANOASTRALAOAQWERLAAERAOQLAQ-AASY 750
 Qy 850 VPSKOSTVTKTQLOFSQYIENRPEM----KQRSIQBDTJKGNBERRAITE 898
 Db 751 QFOADANDMERMALWVLVLRUVS--PEVGHDFESTOALARBEERAIMRPTDALR- 808
 Qy 899 ORKPSBDEVELNGKFDTSQVWGBLALENENQOIDTRAALVEKRLRYLMGTGRNTEE 958
 Db 809 ----QAAALFPALSHTP-WQGRIFTLEQHTEQIARA----GERARAJE 849
 Qy 959 AMMOEWPMI-----VNKNALIRRMNOLSLKEHD--LERRYBNLNREMLA 1006
 Db 850 ALAALFTMUSAGAGLWEEKB--QWLNGALPERLEDPEVVQQRFFTEPEPNALAA 906
 Qy 1007 IEPDKTTRQKRRSCQ----LDELVAL--VNKRDLVRLDQAQKOA----EEBD 1052
 Db 907 ---RITAVSDIABOLIKASPPGKDRIGTOBQLNQWRQFSLLAGKKKALTSAISON 962
 Qy 1053 BHLRTLHQ 1061
 Db 963 YHSLCTETQ 971

RESULT 10
 US-09-949-016-6777
 ; Sequence 6777; Application US/09949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILING REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6777
 ; LENGTH: 1026
 ; TYPE: PRT

; ORGANISM: Human
 ; US-09-949-016-6777
 Query Match 5.2%; Score 285; DB 2; Length 1026;
 Best Local Similarity 21.2%; Pred. No. 2.7e-10;
 Matches 242; Conservative 153; Mismatches 363; Indels 384; Gaps 58;
 ;
 Db 116 DDP--DAEELNPFGDP-----DSEBERTETASPRKTYEDSFYNNSYNPKVEOTPQYL 165
 Qy 79 DGPRSDSVEGSPFRPPSHSAVFDDEKDPIASSGT----YNLDFFDNLVDTFTQTL 130
 Qy 166 NP-----FD-----EPEA 173
 Db 131 EPRASDAKQNOEGKVNTRKSTDSVPISKSTSRLSLSQASDFDGASSGNPEAVALAPDA 190
 Qy 174 FVTIKDSDPPOSTR-KNIRPVDMSKYLADSSKTBEBELDESNIYPKSTPPPNLV-- 230
 Db 191 YTSQSSASSTLKRITKPPPSLK----KOPTKPKTETPPYKETQOPEDRSLVP 243
 Qy 231 --NPVOBLETERVRVKRAP-----PVLSPKT-----GVLN-----E 261
 Db 244 GENLASETKIE-SAKTEGFSPALLETPLEPAVGPKACPLDSESABGVPPASGGGRVQ 302
 Qy 262 NTVSAGK--DLSTSPKPSI-PAPVIGKPNASQSLJWCETVKNYKGUKLTFTSW 317
 Db 303 NSPPVGRKTULPTTAPEAGEVTPRSDGSDGSDPAKGLSV--RUFDSBDK-----SSW 354
 Qy 318 RNLGFSICALHHFRDLDYKSLNPQDIKENNKAYGFAISIGSRLSPSDMVLLAIPD 377
 Db 335 -----DNOQENRPPTKIGK-----PVATMPLEPRPK--MKTPE 387
 Qy 378 KLTWVMTYKVRAMPFSGQBLANVVOEENNSKSTYKVGYETDTNSVDOBKF-YAELSD 435
 Db 388 KLD-NTPASPR--SPASPNDFI--AKGTY--TFDID--KWDDPNFNPSSTSK 433
 Qy 436 LKRSPPELQPIGSAVDELSQDDSYFVNNSGVGSESEHOTPDDHLSRSTAECRRTSD 495
 Db 434 MQESPKLPO-----OSVNFDPD--TCDBSVDPFKNSKTP 466
 Qy 496 TBRQKS----QOSSGRITSGSGDDPGICNTDSQAQVULGKRLKAKTELSDLVNSD 549
 Db 467 SSRSPSPASPEIASBMRANGVGDGL--NKPARK-----KTPLKTDTPFRV--SP 515
 Qy 550 KKCDMSPP-----FCEBETDOKL-----QTDIGSNLEKEL 582
 Db 516 KRSPSLSPDPSSQDPPTAATFTRPPVISAHVATBDEKLAVTNQRWTICMTD--LEAKQ 571
 Qy 583 ENSISLBICSDPSSPIKITSL-STPSKUGYSYRDLDAKKKASLRTQESPDADRTL 641
 Db 572 DYPQP---SDLSTFVNETKFSSPTEELDYNRSYEIBMEKGSSLPODDAP----- 620
 Qy 642 NHADHSKIVOHRLLSQBELKERAVLQBARDALAKGNKHNINTATPPCNQRLSDQ 701
 Db 621 -----KQALYMFDTQSOPSPKSSPYRMSESPTP----CCDS 654
 Qy 702 ODEERRQRERA----RQLTAAEASGVKUNSELPSYGMAMEKLRKSKASGDDN 754
 Db 655 SFESTEALVNTAAKNQHPVGRGLAPNQSHLOVEPKSSOKLEAMGL-----GTPSEA 707
 Qy 755 IRIDNEKEPEGVFGGDELTMLEND----DTPEONSKVNDLKUKLKVRYQ 803
 Db 708 IETTA--PEGSFASADALLSLRHAHPVLSGALDYLSPDLASKNPPFLAQKOBLEFA 763
 Qy 804 PQVANSPSSAAOKAVTSESSQDMKSGTSDLRTSRLOKT----TERFRNP--WPSK- 853
 Db 764 IMRBLAKLQARQALASHSHQDARKRAHPTDYSISKALYSLRIGTAEVKPGILFQP 823
 Qy 854 --DSTVTKTQLOFS-----QYENRPEMKRQSIQBDTJKGMBEKAATETORK 901
 Db 824 DLDLSQTLKARAIITKEREVSEWDKQYBSRREVMEMKIVARVEK----TIAQ 873
 Qy 902 PSBEBVLNGKFKDQSOYVGBLALENENQOIDTRAALVEKRLRYLMGTGRNTEBEMM 961

RESULT 11
US-09-949-016-10870
; Sequence 10870, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10870
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10870

Query Match Best Local Similarity 21.2%; Pred. No. 2.7e-10; Length 1034;
Matches 242; Conservative 153; Mismatches 363; Indels 384; Gaps 58;

116 DDP--DAAEILNPFCDDP-----DSEEPITETASPRKTEDSFYNSYNPKFKEVQTPQYL 165
87 DGRSDSVEGSPFRPSHSFSAVFDKDPIASSGN-----YNDFDNIELVLTQFTL 138

166 NP-----FD-----EPEA 173

139 EPPASDAKNQEGKNTTRKSTDSVPISKSTLSRSLSLQASDFGAGSSGNPRAVALADA 198

174 FVTIKDSPPQSTKR-KNIRPVDMSKYLYADSSKTYBEEELDESNPPYEPKSTPPPNLV-- 230

199 YSTOSSASAATSLKRTKKERPPSLICK-----KOTKKETETPPVKETOQBPDBEESLIPS 251

231 --NPVQELETERRVRVKAP-----PVLSPKT-----GVIN-----E 261

252 GENLASSETKTE-SAKTEGSPALLETPLEPAVGPKAACPLDSBSAEGVUPPASGGGRVO 310

262 NTWSAGK--DLSTS PKESPI-FSPVLFGRKPNAQSOLLYWCKEVTKNTFRGVKUTNFTSW 317

311 NSPPVGKRLPLTTAPEGEVTSDDSGCGEDSPAKGLSV--RLEPDYSEDK----SSW 362

318 RNLGSLPSFCATLHHRPFDLIDYKSJNPQDITKENNKYGDGFASIGISRLLRPSDMVTLAIPD 377

363 -----DNQENPPPTKIGK-----PVAKNPLRKP--MKKTP 395

378 KLTUVTMVLQIRAHFFSGQBLANVVOIENEKSSTKVGVWETDTSVDOEKP--YAE LSD 435

396 KLD-NTPASPR--SPAPNDTPI---AKGTV--TBDID--KWDOPNFPEFSSTSK 441

QY 1007 IEDWKTEAQKRREQLLDBLVALVNKRDAVLDQAQEKAESDEHERTLBONKGK 1066
Db 978 QEQQAHOASLRKEOL-----RVDALERTLEQKKEIE---LTKICDBLIAM 1023
QY 1067 AK 1068
Db 1024 GK 1025

RESULT 12
US-09-270-767-42273
; Sequence 42273, Application US/09270767
; Patent No. 6703391
; GENERAL INFORMATION:
; APPLICANT: Hamburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42273
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-42273

Query Match Best Local Similarity 5.2%; Score 283.5; DB 2; Length 153;
Matches 52; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

442 MQESKLPO-----OSINFED-TODESVPFPKSSKTP 474
496 TEPQKS-----QQSGRTGSSDDGICSMVSDTQAQVLUIGKRRKIAKTFELSDLYVP 549
475 SSPSPSASPFEPIPASAMEANGVGDGGL--NPKAK-----KKPLTKPDRPRVK---SP 523
550 KKDKMSPP-----FIGETDEQK-----OTLGINSIEKEK 582
524 KRSPLSDPQSDOPTPAATSPPPVISAWHITDESKLAVNQKWCMTVD---LEADQ 579
583 ENSRLSLEC RD PESPIKTSIL-SPTSKLGYSYSRDILAKKKHASLROTESDPADRTL 641
580 DYPQP---SLSLTFVNETKRESSPTEBLDYNRYNSYELEYMEKIGSSLQPODDAP----- 628
642 NHADISSKIVQHRLSLRSQBELLKERARVLLFOARRDAALKAGKHNHTATTPFCNRLS DQ 701
Db 629 -----KKQLYLMFTSDSPPVSKVPRVNESESPT-----CSGS 662
Db 702 QDBERROLERA-----ROLBARSEKVKMSLPSYCMAEKURKERSKASBEND 754
Db 663 SPERELBALVNTAAKQHNPVPRGLAFNQBSHLQVPRBKSSQKELBANGJ-----GTPSEA 715
QY 755 FEIDNTNEBTEPGFVUFGGDBLTLNFLNDL-----DTPEONSKVLYKLKQKLEVO 803
Db 716 LEITA---PEGSFASADALISRLAHPVSLCQGADYLEPDIAKNPLFAQQRLQEBLEFA 771
QY 804 PQVANSPSSAAQAVTRESSQDMKGSSTDRLTERIQLT-----TERFRP--WVSK- 853
Db 772 IMRTEALKLKLARQIALASRSHQDAKREAHPTDVSI SKTALYSRIGTAEVKPAQULFOOP 831
QY 854 -DSTVTKTQDQSFS-----QYIENRPEMKRSQBDTCKGNBEEKAETTORK 901
Db 832 DLDLSAQIARABITKEREVSEWKOYKESREVMEMRKVIAEYK-----TIAQ 881
QY 902 PSEDEVLNKGFKDPSQYVQYGEALLENEDQIDTRAVERKLRVIMDTCRNTERBAMM 961
Db 882 MIEDB---OKEVSYSHOTVQOL-VLKBOALADNS--VERS---LADLPRVYKEV L 932
QY 962 QEWMLVNUKGNALIRMMQ -LSLKEHDERRVELL-----NRELRAM-LA 1006
Db 933 EGP---RKNTEVLRCAQBYLSRVTK--EQRQALKHABEKLDRANAEIAQVRGKA 985
QY 1007 IEDWKTEAQKRREQLLDBLVALVNKRDAVLDQAQEKAESDEHERTLBONKGK 1066
Db 986 QEQQAHOASLRKEOL-----RVDALERTLEQKKEIE---LTKICDBLIAM 1031
QY 1067 AK 1068
Db 1032 GK 1033

RESULT 13

US-09-664-958-8
; Sequence 8, Application US/09664958
; Patent No. 6916912

GENERAL INFORMATION:

APPLICANT: Trakht, Ilya
APPLICANT: Canfield, Robert
APPLICANT: Kalantarov, Gary
APPLICANT: Rudchenko, Sergei

TITLE OF INVENTION: NO. 6916912el Tumor-Associated Marker

FILE REFERENCE: 0575/60240
CURRENT APPLICATION NUMBER: US/09/664, 958

CURRENT FILING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 8

LENGTH: 912

TYPE: PRT

ORGANISM: Human

US-09-664-958-8

Query Match : 5.0%; Score 276, 5; DB 2; Length 912;
Best Local Similarity 22.0%; Pred. No. 8.4e-10;
Matches 159; Conservative 103; Mismatches 270; Indels 191; Gaps 33;

QY 289 NASOSLIVWCKEVTKNYRGKVTFTTSWRNGLSFCAILHHFRPDLDIYKSINPODIKEN 348
Db 163 SAKEGGLIWCQRKTAPKYKVNQVHFSWKGDLAFLNIRHRBLIKYDQRKDPTN 222
QY 349 NKKAYD-GFASIGISRLPSPDMYLAIPLDKLTWTLYQIRAHFSGQELNVVOLENSS 407
Db 223 LNNAFEVAKYLDIPKMLDAEDIVNTARPDEKAIMTVSSFYHAFSGQAETETAANRI 282
QY 408 KSTIKVKGNETDINSVDOKEFVAFSLKRE-----PLQOPIGSAVFL 453
Db 283 CTKLAV-NQENGSTIMEDYEKLASLILWIRRITPWDRVPQKTIQEMQKLEDPRDY- 340
QY 454 SODDSVFVNDSGVGESESSEHQTPDDHLSUPSTASPYCRRTKSDEPDKQSOSGRTGSDD 513
Db 341 -----
QY 514 PGICS--NTDSTOAQVLGKK-RLLKAEITLESDL---TYSDDKKDMSPPFICETD 564
Db 353 --CQLBINFNSVOTKARLNRPAMPSGKMSDINNGWQHLEAQKGVEYWLINEIRR 409
QY 565 BOKLQTLDIGSNSLEKEKLENSRSL-BECSDPSPKIKTSLSPLQGKSYSRDILAKKK 623
Db 410 LERUDHL-----AEKERQKASTHEAWTDKGEMKLKRDYETATL-----DIKALTRK 457
QY 624 HASLRQTESDPADRTTLNADHSSKTYVORHLLRSRQEELKERARVILEQARRDAALKAGN 683
Db 458 HZAP--ESD-----LAHODRVEQ--IAASAOHNE-----LDOYD 489
QY 684 KINTNTATPPCNQRLSDQOP-----ERRRQRLRAROLIAEARSGVKMSEL-P-SIGEM 736
Db 490 SHVNTR--C-QKICDQWDALGSLTHSRREALEKTEKOLBA-----IIDQHLRATKP 539
QY 737 AAEKLKERSKASDENDENDIEIDNEP-BEGFVVGGBELNLENDLDP-----PEBONS 789
Db 540 AAPPNWMESEDLODMPVHTBEI-EG-LISHDOPKSTLPADREREALIHPOCG 597
QY 790 KLVLDLKUKKL-----LEVPOVANISSAACKAV-----TESSQDMGSGTEDRT 835

RESULT 14

US-09-664-958-10
; Sequence 10, Application US/09664958
; Patent No. 6916912

GENERAL INFORMATION:

APPLICANT: Trakht, Ilya
APPLICANT: Canfield, Robert
APPLICANT: Kalantarov, Gary
APPLICANT: Rudchenko, Sergei

TITLE OF INVENTION: NO. 6916912el Tumor-Associated Marker

FILE REFERENCE: 0575/60240
CURRENT APPLICATION NUMBER: US/09/664, 958

CURRENT FILING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 883

TYPE: PRT

ORGANISM: Human

US-09-664-958-10

Query Match : 5.0%; Score 274; DB 2; Length 883;
Best Local Similarity 21.6%; Pred. No. 1.2e-09;
Matches 166; Conservative 111; Mismatches 298; Indels 194; Gaps 34;

QY 289 NASOSLIVWCKEVTKNYRGKVTFTTSWRNGLSFCAILHHFRPDLDIYKSINPODIKEN 348
Db 137 SAKEGGLIWCQRKTAPKYKVNQVHFSWKGDLAFLNIRHRBLIKYDQRKDPTN 196
QY 349 NKKAYD-GFASIGISRLPSPDMYLAIPLDKLTWTLYQIRAHFSGQELNVVOLENSS 407
Db 197 LNNAFEVAKYLDIPKMLDAEDIVNTARPDEKAIMTVSSFYHAFSG-----AKOETAA 251
QY 408 KSTIKVKGNETDINSVDOKEFVAFSLKRE-----PLQOPIGSAVFL 467
Db 252 NRICKV-----
QY 468 ESESBHQTPDDHLSUPSTASPYCRRT--KSDTEROKS-QOSGRTGSDD-----PGI 516
Db 262 -QENHLMEDYEKLASLILWIRRITPWDRVPQKTIQEMQKLEDPRDYRVRKPKV 320
QY 517 --CS--NTDSTOAQVLGKK-RLLKAEITLESDL-----YVSDKKDMSPPFICETD 564
Db 321 QEKQOLEBINFNTLQKRLSNRPAMPSGKMSDINNGWQHLEAQKGVEYWLINEIRR 380
QY 565 BOKLQTLDIGSNSLEKEKLENSRSL-BECSDPSPKIKTSLSPLQGKSYSRDILAKKK 624
Db 381 LERUDHL-----AEKERQKASTHEAWTDKGEMKLKRDYETATL-----DIKALTRK 428
QY 625 ASLQTESDPADRTTLNADHSSKTYVORHLLRSRQEELKERARVILEQARRDAALKAGN 684
Db 429 BAF--ESD-----LAHODRVEQ--IAASAOHNE-----LDOYD 460
QY 685 HNTNTATPPCNQRLSDQOP-----ERRRQRLRAROLIAEARSGVKMSEL-SYGEMA 738
Db 461 HNVTR--C-QKICDQWDALGSLTHSRREALEKTEKOL--EADOLHL---EVAKRAA 510
QY 739 BKLKERSKASDENDENDIEIDNEP-BEGFVVGGBELNLENDLDP-----PEBONS 798

RESULT 15
 US-09-091-501B-8
 ; Sequence 8, Application US/09091501B
 ; GENERAL INFORMATION:
 ; APPLICANT: Timley, Jonathon M
 ; TITLE OF INVENTION: utrophin gene expression
 ; FILE REFERENCE: 620-42
 ; CURRENT APPLICATION NUMBER: US/09/091,501B
 ; CURRENT FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03156
 ; PRIOR FILING DATE: 1996-12-19
 ; PRIOR APPLICATION NUMBER: GB 9525962.8
 ; PRIOR FILING DATE: 1995-12-19
 ; PRIOR APPLICATION NUMBER: GB 9615797.9
 ; PRIOR FILING DATE: 1996-07-26
 ; PRIOR APPLICATION NUMBER: GB 9622174.2
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 8
 ; LENGTH: 2008
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (239) .. (250)
 ; OTHER INFORMATION: Description of Artificial Sequence: Chimeric; Xaa = Unknown
 US-09-091-501B-8
 Query Match 4.9%; Score 270.5; DB 2; Length 2008;
 Best Local Similarity 20.6%; Pred. No. 6.1e-09; Mismatches 349; Indels 301; Gaps 53;
 Matches 211; Conservative 164; Mismatched 349; Indels 301; Gaps 53;
 QY 286 RKKENASQSLVWCKEVTKYRGRKINTTSMRNLSCAIIHHRPPLDYSKLSNPODI 345
 Db 148 QQTNESEKILLSWTRQTRPYSQVNVLNFITSWTDGLATNVALVLRHKPDLSIDRVNMP 207
 QY 346 KENNKKAYD-GFASIGISSLERSDMV-----LIAIDDKLT-----VM 382
 Db 208 IERLEHAFSKAHTYLGEKULDPDVAVHLPLXXXXXXXXXXVEVLPQQVITDAIREVE 267
 QY 383 TLYQIRAHPSOBBLN----VQFRENSSKSTKTVGNVETDTWSSVDPQKPYEALSDIKRE 439
 Db 268 TIPRKYKCECEBEIHIQSAVLAEGGSP-----RAETTSIVTEYDMDLDSYQIALE 319
 QY 440 PELQQPISGAVDLSQDD-----SVFNDMSGVR----- 468
 Db 320 EVLTMWLSAEDTFQEDDISDVTVEVKOFOFATHTEMELTAQOSVGSVLAGNQLMTQ 379
 QY 469 -- SESENQTPDHLSPESTASPVCRRKS -----DTEPQKQQS6----- 506

Db 380 GTISBEERFBFIQOMTLNARWEALRVESMEROSRLHDALMELQKQIQLQSSWLTER 439
 QY 507 RTGSDDDPGICSMNTDPOAQVUIGKRM---LKAEKTHLSDL-----Y 546
 Db 440 RIQKESPIGLDDPLPSLO-KLQBHKSLQNDLDEAQKVKNLTHMVVITDENGESATAL 498
 QY 837 -----RLQKTTFRNPFVVFSKOSTVKTQLOQSFSQY---IENRPEM---KROSI 881
 Db 629 QANVUGPWIQTQKMEI-GRISIERANGTL-EDQJSHLKQYERSIVDVKPNFLDIEQKOLI 686
 QY 882 QE---DTKGN-----EKAALTETORKPSDEBVLNGKFQDPSQYVGEALALE 927
 Db 687 QEAJLFDNQHTNYMEHIRUVGWEOLTTARTINEVENOILTRDAKGISOEQMOWFRASP 746
 QY 928 NEQKQIDTRAAVKEKLRYLMGTGRNTEE--ZAMMOBWMLUNKNA 973
 Db 747 NHFTDKHSGCAGLPERPKACLISGYDVERDROGAERFNRIMSLDPMHS 795

RESULT 16
 US-09-091-501B-8
 ; Sequence 8, Application US/09091501B
 ; GENERAL INFORMATION:
 ; APPLICANT: Timley, Jonathon M
 ; TITLE OF INVENTION: utrophin gene expression
 ; FILE REFERENCE: 620-42
 ; CURRENT APPLICATION NUMBER: US/09/091,501B
 ; CURRENT FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03156
 ; PRIOR FILING DATE: 1996-12-19
 ; PRIOR APPLICATION NUMBER: GB 9525962.8
 ; PRIOR FILING DATE: 1995-12-19
 ; PRIOR APPLICATION NUMBER: GB 9615797.9
 ; PRIOR FILING DATE: 1996-07-26
 ; PRIOR APPLICATION NUMBER: GB 9622174.2
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 8
 ; LENGTH: 2008
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (239) .. (250)
 ; OTHER INFORMATION: Description of Artificial Sequence: Chimeric; Xaa = Unknown
 US-09-091-501B-8
 Query Match 4.9%; Score 270.5; DB 2; Length 2008;
 Best Local Similarity 20.6%; Pred. No. 6.1e-09; Mismatches 349; Indels 301; Gaps 53;
 Matches 211; Conservative 164; Mismatched 349; Indels 301; Gaps 53;
 QY 286 RKKENASQSLVWCKEVTKYRGRKINTTSMRNLSCAIIHHRPPLDYSKLSNPODI 345
 Db 148 QQTNESEKILLSWTRQTRPYSQVNVLNFITSWTDGLATNVALVLRHKPDLSIDRVNMP 207
 QY 346 KENNKKAYD-GFASIGISSLERSDMV-----LIAIDDKLT-----VM 382
 Db 208 IERLEHAFSKAHTYLGEKULDPDVAVHLPLXXXXXXXXXXVEVLPQQVITDAIREVE 267
 QY 383 TLYQIRAHPSOBBLN----VQFRENSSKSTKTVGNVETDTWSSVDPQKPYEALSDIKRE 439
 Db 268 TIPRKYKCECEBEIHIQSAVLAEGGSP-----RAETTSIVTEYDMDLDSYQIALE 319
 QY 440 PELQQPISGAVDLSQDD-----SVFNDMSGVR----- 468
 Db 320 EVLTMWLSAEDTFQEDDISDVTVEVKOFOFATHTEMELTAQOSVGSVLAGNQLMTQ 379
 QY 469 -- SESENQTPDHLSPESTASPVCRRKS -----DTEPQKQQS6----- 506

Search completed: May 20, 2006, 17:16:29
 Job time : 60 sec

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model
Run on: May 20, 2006, 17:26:58 ; Search time 186 Seconds
(Without alignments)
Sequence: US-09-856-723A-8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

2097797 seqs, 463214858 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1076	4 US-10-275-595A-26
2	5173	94.2	5	US-10-275-595A-26
3	4485	81.7	882	4 US-10-407-765A-1942
4	3151	57.4	669	5 US-10-450-763-33241
5	1045	19.0	221	5 US-10-450-763-33241
6	1020.5	18.6	957	6 US-11-077-143-39276
7	989	18.0	479	5 US-10-450-763-33240
8	945.5	17.2	1523	4 US-10-473-576-5
9	897	16.3	175	3 US-09-864-761-42978
10	897	16.3	175	4 US-10-029-386-33831
11	510.5	9.3	996	6 US-11-097-143-33565
12	507.5	9.2	1010	4 US-10-359-012-18
13	498.5	9.1	863	4 US-10-359-012-2
14	498.5	9.1	863	4 US-10-359-012-14
15	498.5	9.1	863	6 US-11-169-041-167
16	461	8.4	91	3 US-09-864-761-34415
17	461	8.4	91	3 US-09-864-761-66554
18	441	8.0	1480	4 US-10-359-012-22
19	431	7.9	1026	4 US-10-359-012-23
20	429.5	7.8	904	4 US-10-359-012-16
21	418	7.6	79	3 US-09-864-761-37001
22	418	7.6	79	3 US-09-864-761-66885
23	399.5	7.3	1633	4 US-10-359-012-4
24	368.5	6.7	1004	4 US-10-291-172-35
25	368.5	6.7	1004	4 US-10-221-278-235
26	6.7	1965	4 US-10-359-012-6	
27	6.7	1025	4 US-10-291-172-611	

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1076	4 US-10-275-595A-26
2	5173	94.2	5	US-10-275-595A-26
3	4485	81.7	882	4 US-10-407-765A-1942
4	3151	57.4	669	5 US-10-450-763-33241
5	1045	19.0	221	5 US-10-450-763-33241
6	1020.5	18.6	957	6 US-11-077-143-39276
7	989	18.0	479	5 US-10-450-763-33240
8	945.5	17.2	1523	4 US-10-473-576-5
9	897	16.3	175	3 US-09-864-761-42978
10	897	16.3	175	4 US-10-029-386-33831
11	510.5	9.3	996	6 US-11-097-143-33565
12	507.5	9.2	1010	4 US-10-359-012-18
13	498.5	9.1	863	4 US-10-359-012-2
14	498.5	9.1	863	4 US-10-359-012-14
15	498.5	9.1	863	6 US-11-169-041-167
16	461	8.4	91	3 US-09-864-761-34415
17	461	8.4	91	3 US-09-864-761-66554
18	441	8.0	1480	4 US-10-359-012-22
19	431	7.9	1026	4 US-10-359-012-23
20	429.5	7.8	904	4 US-10-359-012-16
21	418	7.6	79	3 US-09-864-761-37001
22	418	7.6	79	3 US-09-864-761-66885
23	399.5	7.3	1633	4 US-10-359-012-4
24	368.5	6.7	1004	4 US-10-291-172-35
25	368.5	6.7	1004	4 US-10-221-278-235
26	6.7	1965	4 US-10-359-012-6	
27	6.7	1025	4 US-10-291-172-611	

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1076	4 US-10-275-595A-26
2	5173	94.2	5	US-10-275-595A-26
3	4485	81.7	882	4 US-10-407-765A-1942
4	3151	57.4	669	5 US-10-450-763-33241
5	1045	19.0	221	5 US-10-450-763-33241
6	1020.5	18.6	957	6 US-11-077-143-39276
7	989	18.0	479	5 US-10-450-763-33240
8	945.5	17.2	1523	4 US-10-473-576-5
9	897	16.3	175	3 US-09-864-761-42978
10	897	16.3	175	4 US-10-029-386-33831
11	510.5	9.3	996	6 US-11-097-143-33565
12	507.5	9.2	1010	4 US-10-359-012-18
13	498.5	9.1	863	4 US-10-359-012-2
14	498.5	9.1	863	4 US-10-359-012-14
15	498.5	9.1	863	6 US-11-169-041-167
16	461	8.4	91	3 US-09-864-761-34415
17	461	8.4	91	3 US-09-864-761-66554
18	441	8.0	1480	4 US-10-359-012-22
19	431	7.9	1026	4 US-10-359-012-23
20	429.5	7.8	904	4 US-10-359-012-16
21	418	7.6	79	3 US-09-864-761-37001
22	418	7.6	79	3 US-09-864-761-66885
23	399.5	7.3	1633	4 US-10-359-012-4
24	368.5	6.7	1004	4 US-10-291-172-35
25	368.5	6.7	1004	4 US-10-221-278-235
26	6.7	1965	4 US-10-359-012-6	
27	6.7	1025	4 US-10-291-172-611	

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1076	4 US-10-275-595A-26
2	5173	94.2	5	US-10-275-595A-26
3	4485	81.7	882	4 US-10-407-765A-1942
4	3151	57.4	669	5 US-10-450-763-33241
5	1045	19.0	221	5 US-10-450-763-33241
6	1020.5	18.6	957	6 US-11-077-143-39276
7	989	18.0	479	5 US-10-450-763-33240
8	945.5	17.2	1523	4 US-10-473-576-5
9	897	16.3	175	3 US-09-864-761-42978
10	897	16.3	175	4 US-10-029-386-33831
11	510.5	9.3	996	6 US-11-097-143-33565
12	507.5	9.2	1010	4 US-10-359-012-18
13	498.5	9.1	863	4 US-10-359-012-2
14	498.5	9.1	863	4 US-10-359-012-14
15	498.5	9.1	863	6 US-11-169-041-167
16	461	8.4	91	3 US-09-864-761-34415
17	461	8.4	91	3 US-09-864-761-66554
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19	431	7.9	1026	4 US-10-359-012-23
20	429.5	7.8	904	4 US-10-359-012-16
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23	399.5	7.3	1633	4 US-10-359-012-4
24	368.5	6.7	1004	4 US-10-291-172-35
25	368.5	6.7	1004	4 US-10-221-278-235
26	6.7	1965	4 US-10-359-012-6	
27	6.7	1025	4 US-10-291-172-611	

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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4	3151	57.4	669	5 US-10-450-763-33241
5	1045	19.0	221	5 US-10-450-763-33241
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7	989	18.0	479	5 US-10-450-763-33240
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17	461	8.4	91	3 US-09-864-761-66554
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25	368.5	6.7	1004	4 US-10-221-278-235
26	6.7	1965	4 US-10-359-012-6	
27	6.7	1025	4 US-10-291-172-611	

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US07_PUBCOMB.pep.*'
2: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US08_PUBCOMB.pep.*'
3: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US09_PUBCOMB.pep.*'
4: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US10_PUBCOMB.pep.*'
5: /EMC_Celerra_SIDS3/ptodata/2/pubseq/'US11_PUBCOMB.pep.*'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1076	4 US-10-275-595A-26
2	5173	94.2	5	US-10-275-595A-26
3	4485	81.7	882	4 US-10-407-765A-1942
4	3151	57.4	669	5 US-10-450-763-33241

Sequence 5242, Application US/10450763
 Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 FILE REFERENCE: 790C1P/JUS

CURRENT APPLICATION NUMBER: US/10/0450,763
 CURRENT FILING DATE: 2003-06-11
 PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 09/540,217
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: 09/649,167
 PRIOR FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom SEQ ID NO: 53242
 LENGTH: 1023
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DOMAIN
 LOCATION: (254)..(284)
 OTHER INFORMATION: Actinin-type actin-binding domain protein domain identified by Pfam, accession number BL00019D, p-value=4.200e-19,
 OTHER INFORMATION: of 15.33
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 NAME/KEY: DOMAIN
 LOCATION: (237)..(342)
 OTHER INFORMATION: Calponin homology (CH) domain identified by Pfam, accessio
 OTHER INFORMATION: name CH, E-value=2.4e-17, Pfam score of 71.1
 US-10-450-763-53242

Query Match 94.2%: Score 5173; DB 5; Length 1023;
 Best Local Similarity 99.7%; Pred. No. 1..4e-270;
 Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY |||||ADIGNLDDFEDNEDDENRVNQEEKAATITELINKLNFLDEABECDLATNSNPFPDPDAE 61
 61 ADIGNLDDFEDNEDDENRVNQEEKAATITELINKLNFLDEABECDLATNSNPFPDPDAE 120
 |||||AELNPFGDDSEEPETETASPRKTEDSFYNNSYNPKEVOTPOQIINPDFPEAVTICKOS 121
 121 AELNPFGDDSEEPETETASPRKTEDSFYNNSYNPKEVOTPOQIINPDFPEAVTICKOS 180
 |||||RVKKAPAPVPLSKTIGVLENNTSAGKOLSTSPPSPISPVUGRKPNASQSLIUVCKE 241
 241 RVKKAPAPVPLSKTIGVLENNTSAGKOLSTSPPSPISPVUGRKPNASQSLIUVCKE 300
 |||||VTKYRGVKLTNFITSWRNGLSFCILHHRPDLDIYKSLNPDKTKENNKAYGFASTG 301
 301 VTKYRGVKLTNFITSWRNGLSFCILHHRPDLDIYKSLNPDKTKENNKAYGFASTG 360
 |||||ISRLIEPSDMVLLAIPDKLTWMTTYQIRAHPSGQLNLVQIENNSKSTYKVGYETD 361
 361 ISRLIEPSDMVLLAIPDKLTWMTTYQIRAHPSGQLNLVQIENNSKSTYKVGYETD 420
 |||||NSSVDQEKKYAEELSKREPELLOOPISGAVDPLSQDDSVFVNDGGVGSESEHOTPDDH 421
 421 NSSVDQEKKYAEELSKREPELLOOPISGAVDPLSQDDSVFVNDGGVGSESEHOTPDDH 480
 |||||NSSQDQEKKYAEELSKREPELQPIISGAVDPLSQDDSVFVNDGGVGSESEHOTPDDH 481
 481 SPSTASPYCRTKSDTEPOQSQQSGRTSGSDPGICCSNDSTOAVQVLGKRKLAETL 540
 |||||SPSTASPYCRTKSDTEPOQSQQSGRTSGSDPGICCSNDSTOAVQVLGKRKLAETL 540
 |||||ELSPLVYVSDKDKMSPPFICEETDEQKLQTLDGNSLEKELENSRSLECRSPBSPIK 541
 541 ELSPLVYVSDKDKMSPPFICEETDEQKLQTLDGNSLEKELENSRSLECRSPBSPIK 600
 |||||TSLSPTSKLGYSISRDLIAKKKGASLROTESDEDADRTLNHDHSKIVQRLLSQE 601
 601 TSLSPTSKLGYSISRDLIAKKKGASLROTESDEDADRTLNHDHSKIVQRLLSQE 660
 |||||ELKERRARVILEQARRDAALKAGKNKNTATPFRNQLRQDQDERRRQRLRQRLAE 661
 661 ELKERRARVILEQARRDAALKAGKNKNTATPFRNQLRQDQDERRRQRLRQRLAE 720
 |||||ARSGVOMSLPSYGEAMAELKERSKASDENNEIDINNE-PEGFVUGGDBLTLNEN 721
 721 ARSGVOMSLPSYGEAMAELKERSKASDENNEIDINNE-PEGFVUGGDBLTLNEN 780
 |||||DLDTPEQNSKLVLKLUKLEVQPQVANPSSAAQAKATTESSQDMMGGTEDIRTERIQ 781
 781 DLDTPEQNSKLVLKLUKLEVQPQVANPSSAAQAKATTESSQDMMGGTEDIRTERIQ 840
 |||||TTERFRNPFVVFSDKSTVRKTOLOQSSQYTIENRPEMKRNSIQDPTKGSNBKAATTENQR 841
 841 TTERFRNPFVVFSDKSTVRKTOLOQSSQYTIENRPEMKRNSIQDPTKGSNBKAATTENQR 900
 |||||TTERFRNPFVVFSDKSTVRKTOLOQSSQYTIENRPEMKRNSIQDPTKGSNBKAATTENQR 900
 |||||KSPEDEVULKGFKDTSTQYVNGELAALENEQKQDTRALVALVEKLRYLMDGRNTEREFAM 901
 901 KSPEDEVULKGFKDTSTQYVNGELAALENEQKQDTRALVALVEKLRYLMDGRNTEREFAM 960
 |||||MQBWMUJNKNNALLRNMQLSLKENDLERYLLEBLRMLALEDWQKTHAQKRE 961
 961 MQBWMUJNKNNALLRNMQLSLKENDLERYLLEBLRMLALEDWQKTHAQKRE 1020
 |||||QJLLEDVALVALNRKDALYRDLAQEKQABEDEHLERLTLEONKGKACKECKVULQ 1021
 1021 QJLLEDVALVALNRKDALYRDLAQEKQABEDEHLERLTLEONKGKACKECKVULQ 1076
 |||||QJLLEDVALVALNRKDALYRDLAQEKQABEDEHLERLTLEONKGKACKECKVULQ 1076

RESULT 2
US-10-450-763-53242

QY 603 LSPSTSGLGYSISRDJDLAKKHSRQTESPPDARTTLNHAHDHSKIVVORLILSROEL 662
Db 550 LSPTSKLGYISISRDJDLAKKHSRQTESPDADRTTLNHAHDHSKIVVORLILSROEL 609
QY 663 KERARVILLEQRDAALKAGKHNNTATPPCNRQLSDQDPERRQRERQAROLIAAR 722
Db 610 KERARVILLEQRDAALKAGKHNNTATPPCNRQLSDQDPERRQRERQAROLIAAR 669
QY 723 SGVKNSELPSYGEMAAEKLKERSKASGDENDNIBIDTNEPEGFVGGGDELNL 782
Db 670 SGVKNSELPSYGEMAAEKLKERSKASGDENDNIBIDTNEPIPEGFVGGGDELNL 729
QY 783 DTPEONSKLVULDKLKLLBEPQVANSPSSAQAVTESSEQDMGSGTEDLTERLQKT 842
Db 730 DTPEONSKLVULDKLKLLBEPQVANSPSSAQAVTESSEQDMGSGTEDLTERLQKT 789
QY 843 ERFRPUPVFSKOSTRKTQLOFSQYIENPEMKQRSIQDPTKGNEKEAITEQRP 902
Db 790 ERFRPUPVFSKOSTRKTQLOFSQYIENPEMKQRSIQDPTKGNEKEAITEQRP 849
QY 903 SEDDEVALKGGRDTTSQYVGBLALENBOKQDTRALVERKLRYMDTGRNTREBAMM 962
Db 850 SEDDEVALKGGRDTTSQYVGBLALENBOKQDTRALVERKLRYMDTGRNTREBAMM 909
QY 963 EWFMLVNLNKKNALIRRNQMSLKEHDLERYELNRELRAMLATEDWQTCRKEQ 1022
Db 910 EWFMLVNLNKKNALIRRNQMSLKEHDLERYELNRELRAMLATEDWQTCRKEQ 969
QY 1023 LLDELVALVNRKDALVRDLDQEQKABEEDHLERTLBQNGKMAKKEEKVLQ 1076
Db 970 LLDELVALVNRKDALVRDLDQEQKABEEDHLERTLBQNGKMAKKEEKVLQ 1023

RESULT ³
US-10-408-765A-1942
; Sequence 1942, Application US/10408765A
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Robin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glein, Gary M.
; APPLICANT: Watnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660888-465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1942
; LENGTH: 882
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-1942

Query Match 81.7%; Score 4485; DB 4; Length 882;
Best Local Similarity 100.0%; Pred. No.: 1_se-233; Mi smatches 0; Indels 0; Gaps 0;

Matches 882; Conservative 0;

QY 195 MSKLYADSSKTEBEELDESNPPFPYEPKSTPPNPLVNPYOBLETERRVKRKAPPVSP 254
Db 1 MSKLYADSSKTEBEELDESNPPFPYEPKSTPPNPLVNPYOBLETERRVKRKAPPVSP 60
QY 255 KTGVLIENTVSAKDLSTSPPKSPSPVPGRKPMASQSLVWCKTNTYRGKINTP 314
Db 61 KTGVLIENTVSAKDLSTSPPKSPSPVPGRKPMASQSLVWCKTNTYRGKINTP 120
QY 315 TSWRNLGLSFCALIHFPRDIDLDSLNPODIKENKKAvgGASIGISRLPSDMVLA 374
Db 121 TSWRNLGLSFCALIHFPRDIDLDSLNPODIKENKKAvgGASIGISRLPSDMVLA 180

RESULT ⁴
US-10-450-763-53241
; Sequence 53241, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: NOVEL NUCLEAR ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CTP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-01-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 091540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 091649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 53241
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: DOMAIN
LOCATION: (61)...(91)
OTHER INFORMATION: Actinin-type actin-binding domain proteins domain identified
OTHER INFORMATION: by eMATRIX, accession number BL00019D, p-value=4.200E-19, raw score
OTHER INFORMATION: of 15.33
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (42)...(147)
OTHER INFORMATION: Calponin homology (CH) domain identified by PFam, accession
OTHER INFORMATION: name CH, E-value=2.4E-17, PFam score of 71.1
US-10-450-763-53241

CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-05-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/646,9167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 53239

Query Match 57.4%; Score 3151; DB 5; Length 659;
 Best Local Similarity 89.5%; Pred. No. 1e-161; Mismatches 634;保守性 6; Indels 56; Gaps 4;
 Matches 634; Conservative 6; Mismatches 12; Indels 56; Gaps 4;

Qy 248 APPVLSPTGVNLVENTVSAGKDLTS--PKPSPIRSPVGKPMASQSLIWCKETKVY 305
 Db 2 ARPYLYKKYKG--NQGVAALPDVAEWAEPSPISPVLPGRKPNASQSLIWCKETKVY 305
 Qy 306 RGVKITNTTISWNRGLSFCAILHFRPDIYKSLNPDKIENKRNKAYOGFASIGIRL 365
 Db 60 RGVKITNTTISWNRGLSFCAILHFRPDIYKSLNPDKIENKRNKAYOGFASIGIRL 365
 Qy 366 ERSMDMVLIAIPDKLTVMITYQDRAHFSSQBLNTYQIERNNSKSTYKVGETTNTSSVD 425
 Db 120 EPDSMDMVLIAIPDKLTVMITYQDRAHFSSQBLNTYQIERNNSKSTYKVGETTNTSSVD 179
 Qy 426 QBKFYAELSDLKRPELQOPIGSANVDFLSDSVFVNDSGVGESEBEHQTPDDHHSPLSTA 485
 Db 180 QBKFYAELSDLKRPELQOPIGSANVDFLSDSVFVNDSGVGESEBEHQTPDDHHSPLSTA 239
 Qy 486 SPYCRITKSDEQKQSQSGRGSQSGDRGICSTSDTQAQVLLGKRLKAETBLSLD 545
 Db 240 SPYCRITKSDEQKQSQSGRGSQSGDRGICSTSDTQAQVLLGKRLKAETBLSLD 299
 Qy 546 YVSDKKDMSPPFCEETDBQKQLTDGSNLCEKLENSRLCERSDERSPIKTSLSQ 605
 Db 300 YVSDKKDMSPPFCEETDBQKQLTDGSNLCEKLENSRLCERSDERSPIKTSLSQ 359
 Qy 606 TSKLGYSYSSRDLLAKKKHASLQTESDPPADRTLNHADHSKIVQHLLSREELKER 665
 Db 360 TSKLGYSYSSRDLLAKKKHASLQTESDPPADRTLNHADHSKIV----- 405
 Qy 666 ARVILLEQARRDAALKAGKHNNTATPFCNRQQLSDQQDBERRRQRRQAROLIARSGV 725
 Db 406 -----
 QDERRRQDRERARQOLIARSGV 430

RESULT 6
 US-11-097-143-39276
 Sequence 39276, Application US/11097143
 Publication No. US20050208559A1
 GENERAL INFORMATION:
 APPLICANT: Venter, J. Craig
 APPLICANT: et al.
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 TITLE OF INVENTION: DROSOPHILA GENES.
 FILE REFERENCE: C1000728
 CURRENT APPLICATION NUMBER: US/11-097-143
 CURRENT FILING DATE: 2005-04-04
 PRIOR APPLICATION NUMBER: 60/157,832
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: 60/160,191
 PRIOR FILING DATE: 1999-10-19
 PRIOR APPLICATION NUMBER: 60/161,932
 PRIOR FILING DATE: 1999-10-28
 PRIOR APPLICATION NUMBER: 60/164,769
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/181,931

RESULT 5
 US-10-450-763-53239
 Sequence 53239, Application US/10450763
 Publication No. US20050196754A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/911,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SRQ ID NO: 39276
LENGTH: 957
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-39276

Query Match 18.6%: Score 1020.5; DB 6; Length 957;
Best Local Similarity 27.4%; Pred. No. 1.5e-46;
Matches 316; Conservative 166; Mismatches 279; Indels 391; Gaps 38;

QY 1 MKQVQASPMPTQDVKLKKPLSKKVVMSALQQLSCIFRECKATDEDMQSLSLVSMSQ 60
Db 121 MKYKASIESSTSQESTPSLKSKEVSKITAALELTSCFVCFRECKATDEDMQSLSMVSYAN 180
QY 61 ADIGNLDDPFE-- -DNEDDDENRVRNQ----- BEKAAK 89
Db 181 NDVAPlDDEdIPDGFSPBTIDNFDFQOLEMTTSINGCIVATPQSVPSLSEDPIP 240
QY 90 ITELJNKLAFLDRAEAKDLATVNNSPFDDEAARLNPFGPDS----- EBP1-- 135
Db 241 LABESPNNPLP--ELDAGKREBANKKUDLPTAAGCGGSARESLKTPNGLQHVVNDPTIKS 298
QY 136 -TEASPRKTB-DSPTNNSYNPFPKEVQTPQYLNPDEP----- AFVTKDSPPOS 184
Db 299 PEYTKQPKPVESLRSKTEDEPDKWTSPTLPBKPKKKRALPFTED-EKD 357
QY 185 TKRKNIRPVDMSKYLYADSSRSTEELDESNPFPKSTPPNMLVNPNVQBLER----- 240
Db 358 LRVESVEK DTKT-K-GDNSTTKEKPEKPESSQSKDASSVVPSPAKRPELQPNLUKKSTEP 415
QY 241 -RVRKAPAPPVLSPTGTVALENTWSAGKDLSTERPKS---P-PSVPLGRKPEASQIL 295
Db 416 SQTPEASAPV-----ASVINE---SIGCSFTSGSLANSLSKPEVKIVL-KENTPGDILL 465
QY 296 WCKCKEVTKYRGKVKTINFTTSWRKGSLFCMLHNPDLDKYSLNPQDIKENKKAVG 355
Db 466 BWCKCKEVTKYOPNVKVTNLTSWRKGMAFCIAIHNPVPLDMSKLSAHDVGNCRIGED 525
QY 356 PASIGISRLBPSDNVLLAIPDKLJUVTMAYQIRAHFSQBLNTVQIBENSSEKTYKVN 415
Db 526 AELSGIPRVIPEPRDMMLTVFDGLAVMTILQHLAHTFKSKOLKIEQIGSTADESSIVGD 585
QY 416 YETUNNSYVQDQEKEYAELDLKRPPELOPPIGAVDPSQDSDYEVNNSVGGESEHOT 475
Db 586 YKSD-NLSQNRINFSPKSLLHQNSFDRINGS-----N 619
QY 476 PDDHSPSPSTASPYCRTKSDEPKQSQQSGRTSGDDPGCISNTDSTAQVLGKRRU 535
Db 620 KSKQBLSPTE----- 628
QY 536 KABTELESOLSYVSDKCKOMSPPFICEETDBQKLOFTDGSNLERGEKLENSRSLBCRSDE 595
Db 629 -----KKDV-----KKN-----KLN----ILYNSK----- 642
QY 596 SPIKKLSPSKLGGYSYRDLJAKKKHASLQTESDADRT-LTHADHSKLVORH 655
Db 643 -IJDVKVLSPK----- 655
QY 656 LSROBLKLRJARVULQARDDAALKAGKHNINTATPCNRQLSDQO---DRERRQRKRR 713
Db 669 LSCQTPPDSL-----DGKSGPGKGENSIT-----IDPQAERERQRLAQ 714
QY 714 ARQJTAEARSSGVKMSLPSYGMEMAEKUKKERSKASGDENDNITBDTNEBTPEGFVUGGD 773
Db 715 ARRILETR----- 728
QY 774 BLTMLENDLJPTBEONSKLVDLKLKQKLEVOPQVANSPSSAAQAVTESSBDMKSGTRL 833

RESULT 7 US-10-450-763-53240
; Sequence 53240, Application US/10450763
; Publication No. US20050156754A1
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: NOVEL NUCLEARIC ACIDS AND POLYPYRPTIDES
; FILE REFERENCE: 790CP3JUS
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/1649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SRQ ID NO: 53240
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: (419)-(451)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: ematrix, accession number DM01354J, p-value=2.627e-15, raw score 475
; OTHER INFORMATION: 15.12
US-10-450-763-53240

Query Match 18.0%: Score 989; DB 5; Length 479;
Best Local Similarity 67.0%; Pred. No. 3.1e-45;
Matches 209; Conservative 19; Mismatches 50; Indels 34; Gaps 6;

QY 3 QYASP---MPTQDVKL---KFKP-LSKVVMSALQQLSCIFRECKATDEDMQSAS 54
Db 36 OHSPKURQUTPSLHSQGPKKASPAASSEAVASVILPAIGTCMSLGTKLBSA- 94
QY 55 LVSMKQADTGNNLDDFEEDNEDD---ENRVNQBEKAAKITELINKLNPLDEAKLAV 110
Db 95 -VTRAPETVNLQNLASSIDEDQDCIKOAMRSAKSASSEELINKLNPLDEAKLAV 153
QY 111 NSNPEDDPAEALNPFGPDSEREPTEASPRKTEDSYNNSYNPFPKEVQTSQYLNPNPDE 170
Db 154 NSNPFDPPDAEALNPFGPDSEREPTEASPRKTEDSYNNSYNPFPKEVQTSQYLNPNPDE 213
QY 171 PRATVTDSPPOSTKRKNIRPVDMSKVLYAASSKSTEELDESNPFPKSTPPNMLV 230
Db 214 PEARFTKDSPOSTKRKNIRPVDMSKVLYAASSKSTEELDESNPFPKSTPPNMLV 273

PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: GB 242633.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/1236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/1234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO: 42978
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE: OTHER INFORMATION: MAP TO AC007098.2
; OTHER INFORMATION: EXPRESSED IN HILIA, SIGNAL = 0.61
; OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
; US-10-029-386-33831
Query Match 16.3%; Score 897; DB 4; Length 175;
Best Local Similarity 10.0%; Pred. No. 8.1e-41; Indels 0; Gaps 0;
Matches 175; Conservative 1/5; Signal 0.79; Signal Start 1; Signal End 175
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN EST HUMAN HIT: BP307519.1, EVALUE 2.00e-41
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
Query Match 16.3%; Score 897; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
Query Match 16.3%; Score 897; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
RESULT 11
US-11-097-143-23565
; Sequence 23565, Application US/11097143
; Publication No. US20050208558A1
GENERAL INFORMATION:
; APPLICANT: vector, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: PabSeq for Windows Version 4.0
; SEQ ID NO 23565
LENGTH: 996
TYPE: PRT
Publication No. US20030194704A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34388
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 33831
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE: OTHER INFORMATION: MAP TO AC007098.2
; OTHER INFORMATION: EXPRESSED IN HILIA, SIGNAL = 0.61
; OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
; US-10-029-386-33831
Query Match 16.3%; Score 897; DB 4; Length 175;
Best Local Similarity 10.0%; Pred. No. 8.1e-41; Indels 0; Gaps 0;
Matches 175; Conservative 1/5; Signal 0.79; Signal Start 1; Signal End 175
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN EST HUMAN HIT: BP307519.1, EVALUE 2.00e-41
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
Query Match 16.3%; Score 897; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
Query Match 16.3%; Score 897; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P32583, EVALUE 8.10e-02
; US-09-864-761-42978
QY 352 AYDGFASIGISRLEPSDMVLLAIPKLTWMTYQIRAHPSGELNVQIEENSSKTY 411
Db 1 AYDGFASIGISRLEPSDMVLLAIPKLTWMTYQIRAHPSGELNVQIEENSSKTY 60
QY 412 KVGNVETDTNSVSDQKFAVABLSDLKRPELQQPISGAVDPLSODDSVNDSGVGESES 471
Db 61 KVGNVETDTNSVSDQKFAVABLSDLKRPELQQPISGAVDPLSODDSVNDSGVGESES 120
QY 472 EHQTDDDHSPSTASPYCRTKSDEPKOSQSGSGRTQSDDPQCSNIDSTOQ 526
Db 121 EHQTDDDHSPSTASPYCRTKSDEPKOSQSGSGRTQSDDPQCSNIDSTOQ 175

	Matches	218; Conservative	137; Mismatches	367; Indels	153; Gaps	30;
Qy	698	LSDQDEERRQLRERAROLJARANGVYKMSLPSYGMELAKLKERSKAG--DENDNI	755			
Db	437	IPKQMD-----LESPKDKVIB---TKASFTDPBKFDLPPKODSSKCANPFDSSD-	484			
Qy	756	EIDTNEBIP---EGFVVGGDE---LTNLLENDLTPPEQNSKVLVDLKLUKLAVQPOV	806			
Db	485	EVELJKAIPAQSKGRVPPPPPQKIGLSSISNSBKPKHSPTL-SHOKMPMPTPRI	542			
Qy	807	ANSPSSAAQKVWTESSBQDMGSGTEDRTRLQ-KTTERP-----RNP	848			
Db	543	SISKOTTPAKMT---HOGOKSSISSSSEHLNSTRTFDGADRGSSISLPSANGPRKP	599			
Qy	849	VFSKUDSTVRK---TQLOSPSQYIENREPMKQRS--IQED---TRKGNEEK	892			
Db	600	IRASVGSPLSRSSESSPTTSLSITS---PMRKGRQPLPIQTDPSDPGFSKLSDQ	654			
Qy	893	HAITEVORK---PSEDEVINKFKDTSQY-----	918			
Db	655	KALLHTQLKORNGLGSTRRLLPDLQSLSLRATESSNYDLSLTSNADEBENVVYRRLV	714			
Qy	919	------	918			
Db	715	PTQENTVERSKEDOKSPTWYNDPDRNVSPLGHNKSTHGKKWRKGPAAPVTPPKVL	774			
Qy	919	--VUGELAALNEEQKOIDTAALVEKLR-----YMDTG-----RNTER	956			
Db	775	ORLPLOETRHFETTAVOOLQKLGKVGVLKMRDURCERSLDAUTDGPEASVLTNSKE	834			
Qy	957	BRAMMQEWFLVNLVKNGNALLRMNQISLILBEKDERRYLERYELLNRBLRAMLAEDNOKTEAQ	1016			
Db	835	VEDJLQLPELUNGEQELFRKQAEMLYLRQRHLQEQADEIEHTRVLMQPERINKTSD	894			
Qy	1017	KRREQOLLDPEIVALVNLKRDALVLDQAEEKAEDEHHL-----RTL	1059			
Db	895	KAHEEVILNLVKKVEMRNEVIDSLETDRVRAEEDMSIKRHLHYNSREPEPAHPRSA	954			
Qy	1060	BONIGKOMAKERK 1072				
Db	955	DKSSKQLSKKERK 967				
RESULT 13						
US-10-359-012-2						
; Sequence 2, Application US/10359012						
; Publication No. US20030232419A1						
GENERAL INFORMATION:						
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE						
; APPLICANT: KOLODKIN, Alex L.						
; APPLICANT: TERMAN, Jon R.						
; APPLICANT: MAO, Tianyi						
; APPLICANT: PASTERKAMP, Ronald J.						
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPTIDE REFERENCE: JHU1840-3						
; CURRENT APPLICATION NUMBER: US/10/359,012						
; CURRENT FILING DATE: 2003-02-04						
; PRIOR APPLICATION NUMBER: US 60/388,325						
; PRIOR FILING DATE: 2002-06-13						
; PRIOR APPLICATION NUMBER: US 60/384,302						
; PRIOR FILING DATE: 2002-05-30						
; PRIOR APPLICATION NUMBER: US 60/354,178						
; NUMBER OF SEQ ID NOS.: 40						
; SOFTWARE: PatentIn version 3.1						
SBQ_ID NO_ 2						
; LENGTH: 863						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-359-012-2						
Query Match 9.1%; Score 498.5; DB 4; Length 863;						
Best Local Similarity 24.9%; Pred. No. 1.9e-18;						

APPLICANT: YU Hung-Hsiang
 TITLE OF INVENTION: MOLECULES INTERACTING WITH CASI (MICR) POLYNUCLEOTIDES, POLYBP1
 FILE REFERENCE: JHJ1840-3
 CURRENT APPLICATION NUMBER: US/10/359,012
 CURRENT FILING DATE: 2003-02-04
 PRIOR APPLICATION NUMBER: US 60/388,325
 PRIOR FILING DATE: 2002-06-13
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 14
 LENGTH: 863
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-359-012-14

Query Match 9.1%; Score 498.5; DB 4; Length 863;
 Best Local Similarity 24.9%; Pred. No. 1.9e-18;
 Matches 218; Conservative 137; Mismatches 367; Indels 153; Gaps 30;

Qy 293 SLLVWCKEVTNTRGKUTNFTSWRNGISFCATLHFRPDLYKSINPQDIEKKKA 352
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 353 YD-GFASIGISRLIESDMVLAIPDKLTWMTYQIRAHFSG----- 394
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 67 FEVAEKELGIPALIDPDNDMWSVPDCLSIMTVSQYNNHFCSPQAGVSPPRKGLAPCS 126
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 395 -----OELNVVOBENSENSKSTYKVGNNTDTNNS----- 431
 ::|||:|||:|||:|||:|||:|||:|||:|||:
 Db 127 PPSVAPTPVEDVAGEBLSSGSLSEOGTGTGSTCAGCQHVHLVORYLADGRYHR 186
 ::|||:|||:|||:|||:|||:|||:|||:
 Db 432 ELSDLKRPPELQLQPISGAVDLSQDDSVFNDSDVGESSEHQDPDDHLSPSASPYCRR 491
 ::|||:|||:|||:|||:|||:|||:|||:
 Db 187 HCFRCRCCSSTLIP--GAYE-NGPSEGTFVC-----AEHCA---RLGPGTRSG--TR 230
 ::|||:|||:|||:|||:|||:|||:
 Qy 492 TKSDEPOKSQOSSGRTSGSDPGICCSNTDSTOAQVLGKRLIKABTEBLSDLYVSDK 551
 ::|||:|||:|||:|||:|||:|||:
 Db 231 PEPFSQPKQHQOQOLABAQDKVFGGPSSAPAGARAOCPKASPEARQPIKPRVPGKL 290
 ::|||:|||:|||:|||:|||:
 Qy 552 KDM-SPPF-----ICBEDEQKQLOTLIGSMLKEKLU--ENSRLERSDPSPIK 599
 ::|||:|||:|||:|||:
 Db 291 QBLASPPAGRPPTPARKASESTTPAPPTRPRSSLQENLVQAGGSSLVNGRLHLPV 350
 ::|||:|||:|||:
 Qy 600 KTSLSPTSKLGYSYSD---LDA---KKKASLROTES--DPADETTLNHADHSSK 649
 ::|||:|||:|||:
 Db 351 KBRGTPKPESEGTPARKOPWPITLQAEPKKPAPLPPSSSPGPSSPDSRQVENGG--TER 409
 ::|||:|||:|||:
 Qy 650 IVQ-----HRLLSRQEELKERARVLLEQARRODAALKAGNKHNT-NTATPFCNRQ 697
 ::|||:|||:|||:
 Db 410 VAQSPPTASLESKPKYNPTEEEBDKEEBAAPASLATSPL--GHPESTPKSLHPWYGIT 467
 ::|||:|||:|||:
 Qy 698 LSDQDQDERRQERAROLIAFSGYMSLPSGYGMAEKLKRSKASGDENDNIBI 757
 ::|||:|||:|||:
 Db 468 PTSSPKTKRGPAPRAPSPASPLAHSARLISHSEPEPATSPALSVESSLSESASOTAGEL 527
 ::|||:|||:|||:
 Qy 758 DTNEBPEGPVUGGGDELTNLENDTETQONSLVDIUKKLL--VOPQANSSS 812
 ::|||:|||:|||:
 Db 528 LEPPTAVFK-----SSSERPAVHAAGTPGPNVPSLSTNSTJASSGELVRPVEQMQPA 577
 ::|||:|||:|||:
 Qy 813 A--AQKAVTTESSBQDMKGSGTEDLRTBLQKTERFRNPVVFSEKSTDWTKTQLOFSQVYI 869
 ::|||:|||:|||:
 Db 578 SPGLAMRTRGSSGPQPKPCSGATPTPLVNGD--RSPVPSGSS--POIQVKSSCK 631
 ::|||:|||:|||:
 Qy 870 ENRPEMKRQRSIQEDTKKGNEEKATAITETORKPSEDEVLNKGFK-----DTQYVV-- 920
 ::|||:|||:|||:
 Db 632 ENPNRKRPSAASPATKATGOS-----KPVRPARGHGFPLIKRKYQADQYIPEBD 693
 ::|||:|||:|||:
 Qy 921 -GELALENEOKQDITRAALVKKRKLMDTQRNTERREAMQBWFLVUNKGKALIRM 978
 ::|||:|||:|||:
 RESULT 15
 US-11-169-041-167
 Sequence 167, Application US/11169041
 Publication No. US200600192841
 GENERAL INFORMATION:
 APPLICANT: BRISTOL-MYERS SQUIBB Company
 TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER.
 TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER.
 TITLE OF INVENTION: CELLS
 FILE REFERENCE: 10011.NP
 CURRENT FILING DATE: 2005-06-28
 PRIOR APPLICATION NUMBER: US/11-169,041
 NUMBER OF SEQ ID NOS: 527
 SEQ ID NO: 167
 LENGTH: 863
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-169-041-167

Query Match 9.1%; Score 498.5; DB 6; Length 863;
 Best Local Similarity 24.9%; Pred. No. 1.9e-18;
 Matches 218; Conservative 137; Mismatches 367; Indels 153; Gaps 30;

Qy 293 SLLVWCKEVTNTRGKUTNFTSWRNGISFCATLHFRPDLYKSINPQDIEKKKA 352
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 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 353 YD-GFASIGISRLIESDMVLAIPDKLTWMTYQIRAHFSG----- 394
 ::|||:|||:|||:|||:|||:|||:|||:
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 Db 67 FEVAEKELGIPALIDPDNDMWSVPDCLSIMTVSQYNNHFCSPQAGVSPPRKGLAPCS 126
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 Qy 395 -----OELNVVOBENSENSKSTYKVGNNTDTNNS----- 431
 ::|||:|||:|||:|||:
 Db 127 PPSVAPTPVEDVAGEBLSSGSLSEOGTGTGSTCAGCQHVHLVORYLADGRYHR 186
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 Db 432 ELSDLKRPPELQLQPISGAVDLSQDDSVFNDSDVGESSEHQDPDDHLSPSASPYCRR 491
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 Db 187 HCFRCRCCSSTLIP--GAYE-NGPSEGTFVC-----AEHCA---RLGPGTRSG--TR 230
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 Qy 492 TKSDEPOKSQOSSGRTSGSDPGICCSNTDSTOAQVLGKRLIKABTEBLSDLYVSDK 551
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 ::|||:|||:
 Qy 553 YD-GFASIGISRLIESDMVLAIPDKLTWMTYQIRAHFSG----- 394
 ::|||:|||:|||:|||:
 Db 67 FEVAEKELGIPALIDPDNDMWSVPDCLSIMTVSQYNNHFCSPQAGVSPPRKGLAPCS 126
 ::|||:|||:
 Qy 395 -----OELNVVOBENSENSKSTYKVGNNTDTNNS----- 431
 ::|||:|||:
 Db 127 PPSVAPTPVEDVAGEBLSSGSLSEOGTGTGSTCAGCQHVHLVORYLADGRYHR 186
 ::|||:|||:
 Db 432 ELSDLKRPPELQLQPISGAVDLSQDDSVFNDSDVGESSEHQDPDDHLSPSASPYCRR 491
 ::|||:|||:
 Db 187 HCFRCRCCSSTLIP--GAYE-NGPSEGTFVC-----AEHCA---RLGPGTRSG--TR 230
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 Qy 492 TKSDEPOKSQOSSGRTSGSDPGICCSNTDSTOAQVLGKRLIKABTEBLSDLYVSDK 551
 ::|||:|||:
 Db 291 QBLASPPAGRPPTPARKASESTTPAPPTRPRSSLQENLVQAGGSSLVNGRLHLPV 350
 ::|||:|||:
 Qy 600 KTSLSPTSKLGYSYSD---LDA---KKKASLROTES--DPADETTLNHADHSSK 649
 ::|||:|||:
 Db 351 KBRGTPKPESEGTPARKOPWPITLQAEPKKPAPLPPSSSPGPSSPDSRQVENGG--TER 409
 ::|||:|||:
 Qy 650 IVQ-----HRLLSRQEELKERARVLLEQARRODAALKAGNKHNT-NTATPFCNRQ 697
 ::|||:|||:
 Db 410 VAQSPPTASLESKPKYNPTEEEBDKEEBAAPASLATSPL--GHPESTPKSLHPWYGIT 467
 ::|||:|||:
 Qy 698 LSDQDQDERRQERAROLIAFSGYMSLPSGYGMAEKLKRSKASGDENDNIBI 757
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 Db 528 LEPPTAVFK-----SSSERPAVHAAGTPGPNVPSLSTNSTJASSGELVRPVEQMQPA 577
 ::|||:|||:
 Qy 813 A--AQKAVTTESSBQDMKGSGTEDLRTBLQKTERFRNPVVFSEKSTDWTKTQLOFSQVYI 869
 ::|||:|||:
 Db 578 SPGLAMRTRGSSGPQPKPCSGATPTPLVNGD--RSPVPSGSS--POIQVKSSCK 631
 ::|||:|||:
 Qy 870 ENRPEMKRQRSIQEDTKKGNEEKATAITETORKPSEDEVLNKGFK-----DTQYVV-- 920
 ::|||:|||:
 Db 632 ENPNRKRPSAASPATKATGOS-----KPVRPARGHGFPLIKRKYQADQYIPEBD 693
 ::|||:|||:
 Qy 921 -GELALENEOKQDITRAALVKKRKLMDTQRNTERREAMQBWFLVUNKGKALIRM 978
 ::|||:|||:
 RESULT 15
 US-11-169-041-167
 Sequence 167, Application US/11169041
 Publication No. US200600192841
 GENERAL INFORMATION:
 APPLICANT: BRISTOL-MYERS SQUIBB Company
 TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER.
 TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER.
 TITLE OF INVENTION: CELLS
 FILE REFERENCE: 10011.NP
 CURRENT FILING DATE: 2005-06-28
 PRIOR APPLICATION NUMBER: US/11-169,041
 NUMBER OF SEQ ID NOS: 527
 SEQ ID NO: 167
 LENGTH: 863
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-169-041-167

Db 468 PTSSPKTKRPPAPRAPSASPLAHLAHLSHSEPPSATPSPLSVESSLSSASQAGEL 527
 Qy 758 DTNERIPEGFTVGGEDBTLNENDLTPKONSKLUDLKLTLR----VQPQVANSPPS 812
 Db 528 LEPPAVPK-----SSSEPAVHAPGTGPNPVSLSTNSLASSGELVERPVBQMPQA 577
 Qy 813 A--AOKAVTTESSSEODMKSGTEDIKTERLQCTTERRNPVFSKUSTVRKTQLQSFSQYI 869
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 Db 578 SPGLAPRTRESSGPQAKPSGATPPLWGD---RSVPSPGSS---PQLOQTKSSCK 631
 Qy 870 ENRPEMKRORSIQEDTRKGHEKAATTEOPKSSEDEVLNKGPK-----DTSQXWV--- 920
 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
 Db 632 ENPFNRKPSPPASPARTKKATGCS-----KPVRRPAPGKGGPLIKRKVQADQIPEED 683
 Qy 921 --GRBLAULENEQKOIDTRAALVEKURLYMDTGRTVETEERAMMOMQEWFLNKKNALIRM 978
 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
 Db 684 IHGEMDTIERRDALERHGVLVLLBEKURGGINGR---EDOMLVUDWPKLHKGULLVRIE 739
 Qy 979 NQLSLKEKENDLERRYELLURRLAMI-AEDWQTKEARREQOLLDIBVALVNRDA 1036
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 Db 740 SELITYVKOONLEQROADVESELRCILANKPEKDW---TEBDBAREKVLMQSVLTLIEQRNA 797
 Qy 1037 LVRDIDAQEKOAEEDDEHLEFTELONGKOMKEE 1071
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 Db 798 LINCLDBDRORBEEEDKMLR-----AMIKKCB 824

Search completed: May 20, 2006, 17:30:18
 Job time : 193 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on:

May 20, 2006, 17:27:13 ; Search time 11 Seconds

(without alignments)

208.951 Million cell updates/sec

Title: US-09-856-723a-8

Perfect score: 5489

Sequence: 1 MRQYASPPMPTQFDVKLKFKP RTLEQNKGKQMARKERKCVLQ 1076

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US01_NEW_PUB.PEP:*

2: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US06_NEW_PUB.PEP:*

3: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US07_NEW_PUB.PEP:*

4: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US08_NEW_PUB.PEP:*

5: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/PCT_NEW_PUB.PEP:*

6: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US10_NEW_PUB.PEP:*

7: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US11_NEW_PUB.PEP:*

8: /EMC_Celerra_SIDS3_ptodata/2/pubpaas/US60_NEW_PUB.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

26	146.5	2.7	1912	6	US-10-511-937-2561	Sequence 2561, App
27	145.5	2.7	1056	6	US-10-503-928-225	Sequence 225, App
28	145.5	2.7	1212	6	US-10-503-928-201	Sequence 201, App
29	145	2.6	3396	6	US-10-505-928-449	Sequence 449, App
30	144	2.6	1575	6	US-10-503-928-257	Sequence 257, App
31	142.5	2.6	284	6	US-10-503-928-447	Sequence 447, App
32	141.5	2.6	586	6	US-10-505-928-314	Sequence 314, App
33	140.5	2.6	1066	6	US-10-511-455-2	Sequence 2, App
34	139.5	2.5	1066	6	US-10-370-959-2	Sequence 2, App
35	139.5	2.5	1066	7	US-11-303-678-50	Sequence 50, App
36	139	2.5	1050	6	US-10-503-928-347	Sequence 347, App
37	137.5	2.5	783	6	US-10-511-937-2985	Sequence 2985, App
38	135.5	2.5	823	6	US-10-511-937-2946	Sequence 2946, App
39	132	2.4	1395	6	US-10-503-928-513	Sequence 513, App
40	129.5	2.4	2351	7	US-11-183-218-30	Sequence 30, App
41	128	2.3	284	6	US-10-503-928-670	Sequence 670, App
42	128	2.3	1193	6	US-10-503-928-537	Sequence 537, App
43	127.5	2.3	1066	6	US-10-511-937-801	Sequence 801, App
44	126.5	2.3	502	6	US-10-511-937-3008	Sequence 3008, App
45	126.5	2.3	2351	7	US-11-280-757-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-10-972-140-1
Sequence 1, Application US/10972140
; Publication No. US2006008892A1
; GENERAL INFORMATION:
; APPLICANT: Wear, Ilona F.
; APPLICANT: Yang, Shu-Ping
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Detection of Trichomonas
; FILE REFERENCE: 1441.168051
; CURRENT APPLICATION NUMBER: US/10/972,140
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Trichomonas vaginalis
; US-10-972-140-1

Query Match 4.7% ; Score 255.5; DB 6; Length 849;
Best Local Similarity 20.6%; Pred. No. 5.2e-10;
Matches 170; Conservative 152; Mismatches 285; Indels 219; Gaps 43;

Result No.	Score	Query Match Length	DB ID	Description
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2	233	4.2	2871	6 US-10-505-928-00
3	223.5	4.1	3113	6 US-10-505-928-325
4	222.5	4.1	915	6 US-10-523-014-4
5	213.5	3.9	919	7 US-11-251-465-31
6	212	3.7	2829	6 US-10-525-462-1
7	185	3.4	3256	6 US-10-505-928-357
8	184	3.4	1120	6 US-10-505-928-213
9	182	3.3	1384	6 US-10-505-928-799
10	180	3.3	1674	6 US-10-511-937-2587
11	167	3.0	4373	7 US-11-118-522-2
12	166	3.0	301	7 US-10-511-937-2597
13	164.5	3.0	671	6 US-10-196-749-346
14	164	3.0	1610	7 US-11-252-276-22
15	162.5	3.0	186	6 US-10-511-937-2566
16	162	3.0	1125	7 US-11-252-276-152
17	159.5	2.9	1234	7 US-11-327-900-6
18	157	2.9	638	6 US-10-511-937-2610
19	154.5	2.8	1531	6 US-10-505-928-217
20	151	2.8	769	6 US-10-522-043-9
21	150.5	2.7	730	6 US-10-505-928-841
22	150	2.7	798	6 US-10-511-937-2451
23	147.5	2.7	663	7 US-11-169-140-14
24	147.5	2.7	1809	6 US-10-559-415-2
25	147.5	2.7	1919	6 US-10-559-415-2

QY 620 AKKGHASURQESTPPADRTILNHADHSKIVOHRLSROELKERAVILLEQARDAL 679
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 440 VELRINTL-SSQUDSVN-----HISQOLTY-----IKHIEQLNGKLSEETNEARI 486
 QY 680 KAGKHNTNTATPCNQLSDQQDE-ERRQRERARQLTAARSGVKNSLSYGYEMA 738
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 487 --NEYNA-LAQPIYDEIAFKPCKVLAISGEAERRTQFLA-----KQAEAPT---KR 532
 QY 739 EKUKERSKA-SGPBENDNBIDTBEBIPCGFVVEGGDELINLENDLTPEONSKVLCLK 797
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 533 EHNEIDPFDGKEDSHLHLRVNH-----SPEIRANVAVTLOH---ITBLN 577
 QY 798 KILLEQRPQVANSISSAAQ---KAVTESSEQDMKSGTBDLTERLQTERFRNPWVFS 852
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 578 KIFB--EMVAFDAPTAVPIDGITALVTSOSH-----IP 609
 QY 853 KOSTVRKIQOLQSQYIERPENMRQSTSQDTKGNBKAITETORPKPSDEVLNKG 912
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 610 GDAAVKQVTE-----ENLASCDCVRR-KDPPSPGSJORARSIQAQL-----I 651
 QY 913 KDRSOY--VUGELAJALENEOKOIDTRALIVEKURLYMDTGRTBEEARMQDFWMF--- 967
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 652 KVTVTYSDATGELV-----QARUDLQQTILLAKK-----TFLEEBERKARINNYTVKADE 700
 QY 968 -VNGKGNALLRMQOLSLKEHDLERVELLNRLRAM-LAIEDWQTKBQKREQLL 1024
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 701 HMMTEAHALDGKINSVVD-GRBLEPKRQKLYB-VREBUNAKKEKAVEELTPIYDLEKDOHLL 758
 QY 1025 -----DELVALVNKDALVALVDDAO---EKOAEBEDEHL 1055
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 759 EITSTPASINNPFENLIH-----DTLVKEIDARIAAAGLE-SEBEL 802

RESULT 2
 US-10-505-928-100
 ; Sequence 100, Application US/10505928
 ; Publication No. US20060088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505, 928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/363, 019
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO: 100
 ; LENGTH: 2871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-505-928-100

Query Match 4.2%; Score 233; DB 6; Length 2871;
 Best Local Similarity 18.4%; Pred. No. 1e-07;
 Matches 164; Conservative 164; Mismatches 297; Indels 266; Gaps 36;

QY 343 QIKENNKAYGPGFASTGIRSLRPSMVLAPDKLUTMTYQRAHPSQELNVOI 402
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 1129 ERFDQOKNDY---QIKAROCCEKENIGWQKLESBSKAKEKEYE-----ERLRYVHQ 1179
 QY 403 EENSSKSTY---KVGNYETNTSSUQEKFAELSDLK---REPLOQP----ISGA 449
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 1180 RGGTRKREBYENLAKVRHYNEMSIL-RNKYETEINITKT-TKEISMOKEBDKSLNLRQ 1238
 QY 450 VPFLS-----ODDSVFNDSGVGESESSEBQTPDDHLSPTSPASCPRTKSITPEOKSQ 503
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 1239 IDRISRENRLDKEIVRLNDLQATEOR-----RRAEENALOQA-- 1279
 QY 504 SSGRTSSEDDPQICSNSTQDQVLUKGKRLKAETLBSIDYVSDKRDMSPPFCET 563
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 1280 ---COSB-----IMQKQHIBELQVMQRSSEDNARH----KQS 1312

RESULT 3
 US-10-505-928-325
 ; Sequence 325, Application US/10505928
 ; Publication No. US20060088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505, 928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/363, 019
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO: 325
 ; LENGTH: 3113
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-505-928-325

Query Match 4.1%; Score 223.5%; DB 6; Length 3113;
 Best Local Similarity 19.3%; Pred. No. 4.9e-07;
 Matches 237; Conservative 215; Mismatches 486; Indels 293; Gaps 53;

QY 41 EKGATDMDMOSIASVMSMQADIGN-DPDEFBDNE-----DDENRVQSEKA 89
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 Db 1572 QIMMKONGIQSBLQUSRBBLDCRKYQIISBNBQKUTSVTLEMESKLAECQCTE 1631

```

RESULT 4
US-10-23-014-4
; Sequence 4, Application US/10523014
; Publication No. US20060094101A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Lih-Ling
; TITLE OF INVENTION: MK2 Interacting Proteins
; FILE REFERENCE: 08702-0097-00304
; CURRENT APPLICATION NUMBER: US/10/523,014
; CURRENT FILING DATE: 2005-02-01
; PRIORITY APPLICATION NUMBER: USSN 60/400,044
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-523-014-4

Query Match          4.1%; Score 222.5; DB 6; Length 915;
Best Local Similarity 24.5%; Pred. No. 9.5e-08;
Matches 100; Conservative 66; Mismatches 175; Indels 67; Gaps 15;
Oy      6 SIMPTQDVKFKPKLISKVVAISALQFLSLCIFLAGKATBDMQSILASVMSKMKDIGN 65
Db      533 APPSSRGCCSIKMEPPAPLAAVRAANGABQTRUNKA-PGRSFLSABLMITDEGV 591
Oy      66 LDPFREUNEDDENRQNQQEAKATTEL-INKLNFD-EAKDILATVNSPFPDDDAEL 123
Db      592 LDKMLDOSTDFBERKLIR---AALKEBLRQKRDKERBRRLQBARGRGPE----- 640
Oy      124 NPFGDPPSEBPETETASPR-----KTEDSFYNNSYNPFFKVQPOYLNPFDEPE 172
Db      641 --GRNTATETTTRISQRADGSAVSTVTKTERVHSNGCTRRTTVE-----S 689
Oy      173 AFTVTKDSSPPOSTKRKNRIPVDMSKYLADSSKTRBEELDESNPFPYEPKSTPPPNVLNP 232
Db      690 SFVRRSANGGSTM-----MQTKTFSSSSKKMGSIFDR----EDQASPRAGSLA-- 736
Oy      233 VOELETERRVERKAPAPPVPSPKPGTLN-----ENVSAGKDLSTS PKPSI PSPV 283
Db      737 --ALEKROAEKKELWKAQSLPKTSASQARKAMTKEKLEKKGAA---PGGPRAAVORYSTS 792
Oy      284 LGRKPNAAS--QSLIVPKWCKTENYGVKTNFTTSWRNGLSFCALIHLHRPDLDIKSL 340
Db      793 FG-VPMNASTIKQMLJLWCRAKTRGYEHVDIQNPFSSSWSDGMACFLVHNFPEAFDYGQL 851
Oy      341 NPQDIEKNNKRAYDGFAA-1GSRLLPESDMVLLAIIDPKLTUVTMYYQ 387
Db      852 SPQRNQKQNPFEVAFSSAETHADCPQMLTDMDVRLRPEPDWKCVTYIQB 899

RESULT 5
US-11-251-465-31
; Sequence 5, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandghinate, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And

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TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30.172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31
LENGTH: 919
TYPE: PRT
ORGANISM: Homo sapiens
US-11-251-465-31

Query Match 3.9%; Score 213.5; DB 7; Length 919;

Best Local Similarity 21.7%; Pred. No. 3.9e-07; Mismatches 246; Indels 225; Gaps 34;

Qy 436 LKKRPELQLQPISGAVDPLSODPSVFDVNGVGEGESERHOTPDHLSPTASPCRRTGS 495
Db 152 LTKKE-----DNHTQCLVPUVREGI---SERONAOVTOLMSTPLPRTLSP 198

Qy 496 TEPOKSQQSSGRITSGSDDGICNSNTDSQIAQVLGKKRLKAETL----- 540
Db 199 TAPASATAPISQGPISTD-----ESTK---SKARLESITVSLIMATQDPKGQCV 248

Qy 541 -----ELSDLVYSDKKDMSPPPICBETDBOKLTL-----DIGSNLBGEKLENSR 586
Db 249 GTGRSASKLRIAQVSPGPDR-SPAPPDSPWRERVLAIPILPDNFSTPTGSRTSQVRH- 305

Qy 587 SLECRSDPESPKKTSLSSTKIGSYSSDLDIAKKHSLR-----QTESDPADR 638
Db 306 -----SPIASPPSP-QVLAQKS---LYAKOSSVVRRASRLLAKTAAPEA-- 349

Qy 639 TTINHADHSKSIQH---RLI-----SROBLERKARVILBEQARDHALKAGIK- 684
Db 350 -----SGRICHSYLVERLAVEVPKQKVSGSKEPPEAEV-VAALEPEVHENNGINS 400

Qy 685 -HN-----TNTATPFCNHO-LSDQDPERERRQLRERAROLIAABRSGV 725
Db 401 WPHNDTEIANSTNPKPAAASSPSTSAGQOEAKTDQADGPREPPOSARKRSYQA--- 456

Qy 726 KMSRLPSYGEMMAEKLK-ERSKASGDENDNIEIDTNEELPEPGVNGGDELTMILENDLT 784
Db 457 -VSBLDEEOHLEDELOPRSKT-----PSSPCPASKV-----RPLRTFLT 498

Qy 785 PEONSKVUDLKLUKKELEVPOQVANSPSSRAQAV-----TSESEQDM--- 826
Db 499 VORNQMLM-----TPTISAPTSYKSFTRKNTLIRMDPKEKQRQLRLENTR 542

Qy 827 -KSGTEDIRTERLQKTERFRNPVVFSKOSTVRKTQLOFSFSYENREMKHQ---RS 880
Db 543 RKEEABOLRQKVEEDKERRLEVKKREERLKV-LOARERVEQMKEBKKQIEQPAQ 601

Qy 881 IGDFTKGNKEKAIATEPORKOSSEDEVINKGFKDTSQTVGELAALENEQKQDITRALV 940
Db 602 IDEKTEKAKERLAEKAKKK-----AAAKKMEVEARRKQE 638

Qy 941 E-KRURVLMDFGRNTERERAMQOBWFLVNKK--NALIRRNQSLILEKSHDLR-Y 994
Db 639 EDARRRLWLOQ---EEFERRIHQ---ILQKUGEEDEBLRKAEEAKRLABREBEEQ 691

Qy 995 ELANRELGRMALTEDDWQKTEAKQKREQOLLDSLVALVNKRDAVLRDIAQEQQAEERDEH 1054
Db 692 ERREQERERREQERERREQERERQERERQERERQERERQERERQERERQERLOAERLOBERECAERLOKEQ 751

Qy 1055 LRTTLEONGKGKAWKKEK 1072
Db 752 LQRELEBKK---KCKEQ 765

Sequence 1, Application US/10525621
Publication No. US20060100418A1

GENERAL INFORMATION:
APPLICANT: Kiyosue, Yuko
APPLICANT: Sasaki, Hiroaki
APPLICANT: Tsukita, Shoichiro
APPLICANT: Eisai Co., Ltd.

TITLE OF INVENTION: CULTURED XENOPUS LAEVIS CELL LINES
FILE REFERENCE: 082368-002400US
CURRENT APPLICATION NUMBER: US/10/525,621

PRIOR APPLICATION NUMBER: PCT/JP03/10434
PRIOR FILING DATE: 2003-08-19
PRIOR FILING DATE: 2002-241487
NUMBER OF SEQ ID NOS: 9

SEQ ID NO 1
LENGTH: 2829

TYPE: PRT
ORGANISM: Xenopus laevis

US-10-525-621-1

Query Match 3.7%; Score 202; DB 6; Length 2829;

Best Local Similarity 18.1%; Pred. No. 1.2e-03; Mismatches 433; Indels 438; Gaps 52;

Qy 66 LDJPFEDNEDDDENRVAQVQBEKAQAKITELINKUNFLDE-----EKOLATVNSNPFDPP 119
Db 1134 VDYDDDDCTINSERVYSEEQQDETETRQNKNKAYASEEHGEQPIDYSRKYSTDVS 1193

Qy 120 AAEINP-----GPDSPSERITEASPRKTEDSFYNNSTNPKEVOTPOYLNPFDEP 171
Db 1194 SAQKPSFFPSNNNSKQKKEQVSSNSNTPSPNSNRQNLHPLNSAQSRPGLNRPQKIP 1253

Qy 172 EAPTIKSDPPOSTKRNIR-----PVDMSKYLVADSSKTBEEBD-----ESN 215
Db 1254 -----NKPPSINOETIOTCYVEDATPICFSRGSSLSLSSADEDRGERNSRGQESN 1305

Qy 216 ---PFYBPK---STPPPNNLVNPVOELETERRVR-----K 245
Db 1316 NTQQTIEKEISAVSKQGAVNTRSSVHTRKNNLQTSNIPSQDSSRHSKEVFPSSAK 1365

Qy 246 AP-----APP-----VLSPTKGVAMENTVS--- 265
Db 1366 SPKSGAQTPKSPPEHYQETPLMPSRCTSGSSLSDSFESHSTASSIASVASHEMHMSGII 1425

Qy 266 AGKDLSTP-----KPSIIPSPVIGKRNQASQSLVNCKEVTKYGVKINTPTS 316
Db 1426 SPSPDLPSPGQMPPSRSRKTPPPQPTVQAKDGS-----KPIVDEERGKV--TA 1475

Qy 317 WRGLSLFCAILH-----HFRPLDLYKSLNQDIKEKKAYGF--ASIGISRLP 367
Db 1476 VHSAIQRVQVQLQBADTILHA-----TESTPDGSCASSISALSIDEP 1518

Qy 368 ---SDMWVIALTPDKLTWMTYQIRAHSGOBINVVQIE---ENSSKSTVKGNYBTDT 420
Db 1519 YIQDKVQKIMPVL-----ENDOGNAKEPEKESFDIKAKKEDKRSEQBDKM 1565

Qy 421 NSSVDQSKFYAR---LSDKQBP-----ELCOPISGA----- 449
Db 1566 LDDPDDPDTLRECISAMPKPSRKPKNKVQPTPKSPQPLVQYKLSSQR 1625

Qy 450 -----VPLSODD-----SVFVNDSGGVBSEHQTPDHLSPSTASP 487
Db 1626 LQTKRKHFTSDMDPVCYCTPINSTATSLSLTIESPPSE-----PTNDQ 1676

Qy 488 YCRRKSTDEPORKQSOSGRITSGSDDGICNSNTDSQIAQVLGKKRLKAETLSDLYV 547
Db 1677 NTDSLSTLDEKRDTIPTGR-----STDTDASKFLNPTVLDLDEKAEGDIL 1725

Db 1726 BCIRHAMPKGKSHKPKTRVKKMDQ-----INHSAATSGNSRSMOTDRNKPSPV 1778

Qy 600 -----KTSIISPTSKUGYSRSRDLAKKTHASLQTESPPDRTTINH 643

Db 1779 PMPQSITGPKERLKKTTELKLNPNSENOYCDPRK--PSSKPKPSVANEKIPNNERHTKGF 1835

Qy 644 ADHSKIVOR-----LLSRBL-----KERAVILLEQARRDALKA 681

Db 1836 AFDS---PHYTPIEGTPCFSRNDSLSSLDPEDDIDISKERKELKRGTKTDQKV 1891

Qy 682 GNKHNNTAATPCNQLSDODDEERROL--RERRAROLIAEARSQVMSLPSVGRMAAB 739

Qy 1892 KTKHNRAINM----GRQDQTPRSLGAGDKRDPKALV-----OKPTSSAAK 1935

Qy 740 KUKERSKASGDENDVIRIDTMEBPGFVGUGDILNLNDLPPEQNSKLVJULKLU 799

Db 1936 GTQDRGGATDKMENFAI--ENTPVCF--SRNSLSSL-SDIDOBENNNGTEPLK--- 1985

Qy 800 LEVQOQVANSSAQAKAVTSSEDQMSGSTEDLTERLOKTTFRNPVPSKOSV 859

Qy 1986 -----QTCISBTQGLURRPQTSGYKPSFVED-----TPCPSSANLSS 2026

Qy 860 TOLOSFSQYENRPMKRSQSTIOBETKKGNTEKAJAITETORKPSBDEVANKGFKTSORY 919

Qy 2027 LS1SDBDLL-----QECISSAMP-----KRKPS--K1KNEVGKRSNSV 2065

Qy 920 VGEMLALENQOKOQITRAALVERKRYLMGTGRNTTBBAMMO---EWPMUWKKNAL 974

Db 2066 GGIL-----EBEDLTBLRDI-----QSPDFSPSSENPOKAIQBGANSI 2110

Qy 975 IRMMQQLSLIKEHDLERRYELLNRLRAMIAEDWQTEAQKREBOLLDLVAL--V 1031

Db 2111 VSLHQAA-----AAGSLSRQSSSDSISILSGI 2141

Qy 1032 NKRDALVRDLDAQEQKQAEEDBEHLRTBLONG--RMAKKEKECVQ 1076

Db 2142 SLGSPFHFLTDKEK-----TITSNKGPKILKPAEKSALE 2176

RESULT 7

; Sequence 357, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILM REFERENCE: 2896739178

; CURRENT APPLICATION NUMBER: US/10/505, 928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363, 019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO: 357

; LENGTH: 3256

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-505-928-357

Query Match 3 4%; Score 185; DB 6; Length 3256;

Best local similarity 19.1%; Pred. No. 0.002; Matches 231; Conservative 163; Mismatches 470; Indels 344; Gaps 52;

Qy 2 KOYASPMPT---QTVK-LKPKPLSKKVVSAALPSLSCIFLRSGKATDBDMOSIASLVS 57

Db 1172 KAMLPKPGAGEDEKOKIAKAFMGTPVVKUDLAGTLPESS---KROQTPKKAQMLEDLAG 1226

Qy 58 MKQ-----ADIGNLDDPERDNBDD-----ENRVQOQEKAKIT-ELINKL 97

Db 1227 FKELIQTGHTBELVAAGTKTAKIPDSDPVDPTSTKQRPKSIRKADVEGELLACR 1286

Qy 98 NFLDRBAAKOLATVNNSPFDPPDAEELNPFGDPDSESEPIE--TASPRKTEDSFNNNSYMP 155

Db 1287 NMPSAGKAMHTPKPSVGEKDIIF--VGTPVOKUDLNTENLTSKRPQ-----TP 1336

Qy 156 KFEYQTPQVIANPFB-----PEAFVTK-----DSPQ-----STKRENTPV- 193

Db 1337 KEEAGALEDITGKELFQTPGHTHEAVAAGKTTKWCSSPESADTPSTRQKPTPL 1396

Qy 194 --DISKYLIA-----DSS-----KTBELDLSNPFPYRSTP 225

Db 1397 KRDYQKELSLAKKUTQTSGETHTDKVPGGBEDKSINAPETKOKLDPJASVIGSKRHK 1456

Qy 226 PNNUVNPVBL-----ETERRVKRKAAPPVPLSPKIG----- 257

Db 1457 TEKAQPLEDLAGWKLFOQTPVCTDKPPTHEKTKLACKSQPDVTPSKPSKRSLR 1516

Qy 258 -----VLANETVUSAGKDLSTS PKS P S P V L G K P - N A S O S L U W C R E V T K N T G 307

Db 1517 KVDEBEFFALKRKTPSAGKMT-PKPA---VSGEKNIYAMGTPVOKDLTNTG 1570

Qy 308 VR-----ITNP-----TTSWRNGLSFCATLHHFRPDLDIYKLM 342

Db 1571 SKRRLQTPKREKAQALDEDLAGPKELFQTRGHTESMNINDKTAVACKSSQPDL---DKP 1626

Qy 343 QDIKENNKAYDGASIGSRLJEPSPDMVTLAIPDKLTWTLYQIRAMFSGOBLNV-- 399

Db 1627 ASSKRKLKS--LGKVGVR-----BLIAV-GKLT-----QTSGETHTHTB 1665

Qy 400 VOIEENSSKSTIKVGYNEYDNTNSVDOQEKFYABSLDKRBPLOQPIGSAVDFLSQDDSV 459

Db 1666 PTGQCKSMKAFMBSPKQIIDSASLTGSK--RQLRTPKKSVEPDLAGFTE-----L 1716

Qy 460 FVNDSGVGSESEHOT-----PDDMUSPSPASPCRT--KSDBPO---KSOQ 503

Db 1717 QTFSHTKSWMNTNEKTIKVSYRASQPDLVDTPTSKPKQPKRSLRKADTBBLFLRKQTP 1776

Qy 504 SSGTRGSGSPDPGCSNTST-----QAOVLSKRL-----KAETLB----- 541

Db 1777 SAGKAMHTPKPAGBKEKDINTFLGTPVQKUDQPNLPGSNRQLQTRKEKAQALBELTGF 1836

Qy 542 -----LSDIVYSDKKDMSPPFICETEDEQKQLOLTDIGSNSLKEKLENSRSIERSCRSDP 595

Db 1837 BLFQTPCTNPTADEK--TTKTLCKSQS-----DADPTPTKQPKRSRSLKADVE 1888

Qy 596 SPIKETSSP-----TSGKLYSYSRD-----LDAKKKHSILQPSRSPDAD 637

Db 1889 BFLAPRKLTPSAGKAMHTPKAVERAGEBKEKDINTFLGTPVKEKDLGLNLPGSKRQTPKES 948

Qy 638 RT-----TLNHDHS--SKI VORHLSROB-----LITERAVILLEQAR- 674

Db 1949 KALEDLAGFKELFQTPGHTESMWDKITEVSKCSPQDPVCKPTSSKORLKSILGV 2008

Qy 675 RDAALKAGKHNNTATPCNQLSDODDEERROLRARRQOLIABARSQVMSBLPSV 734

Db 2009 KEEVLPGVGLTQTSGKTTQHTRSTAG--DGKSIAKFAKESAKQMLDPAVGTGMRWPPTP 2066

Qy 735 EMALAKLKRS--KASGDENDNIEBTDTMEBPGFVGUGGDBL-TNL-----ENDLDP 786

Db 2067 KEEAQSLEDLAGFKELFQTPDHTESTD-----DCTKIAKCKSPPPESMOPPT 2115

Qy 787 QNSKLVQDCLKLKVQOQVANSSAQAKAVTSSEDQMSGSTEDLTERLOKTTER 846

Db 2116 STRPKPKTLGKRDIVE-----ELSALKQIQTHTDKVPGDDEBKQINVFETAKQKL 2168

Qy 847 NPVVFSKUSTVKTQLOQESPSQYENRPMK--ORSIODETKKGNEOGAI----- 895

Db 2169 DPAASVTSKQRTPKPSKAQPLEDLAGKELFQTPVCTDKPPTHEKTKIACRSPQDP 2228

Qy 896 --TETRKESSEDEVANTKPKFTDQYVWGLALNEOQIDTAVALVERKRYLMDTGCRN 993

Db 2229 VGTPTPKPOS KSLR-----ADVEEESLALRKRTPSVGMAMTPKPGGD 2275

Qy 954 TEEBAMM 961

Db 2276 EKDMKAFM 2283

RESULT 8
US-10-05-928-213
; Sequence 213, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 213
; LENGTH: 1120
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-213

Query Match 3.4%; Score 184; DB 6; Length 1120;
Best Local Similarity 18.9%; Pred. No. 4.9e-05;
Matches 232; Conservative 188; Mismatches 444; Indels 364; Gaps 56;

Qy 28 ALOFLSLCIFLRKGKATDEMQSLASLUVSMQADIGN-----ADDPEEDNEDDE 78
Db 47 SLSLPI|S|L|G|LQG---SNNSPVDPE|T|NKTKRDLSSBHFSSKWLTCQHESDPL 102

Qy 79 NRVNQBEKAAKTE-----LINKUNFLDABEKO-LATVNS---N 113
Db 103 DPTIQISSLSPKTSBEAVDPLIGNMVKTVLVLPSLQGQQDMIEARLTMTAENNSLING 162

Qy 114 PF--DDPDAAELNP-FGD----PDSEPRITERASPRITEDSFYNNNSYNPFKEVQTOY 164
Db 163 PLRTTDDLVREEVACMGDRPFSKEVAVSEKPIFO-----ESPH 200

Qy 165 LNPDPDEPEAVTIKDSPOSTKRKNIPUDMSKLYADSSKTREEEL-DESNPPYERKS 222
Db 201 L-----LRSPEPVCSE---LHSCKSLSRTERTAEVREDVPSSENAPL-PSS 244

Qy 223 T---PPPN-----NLNVNPVOBLETERRVKRKAPAPPVLSPKTGVLMENTVSAGKD-L 270
Db 245 VMLSLSPSTALADEPRVNTDPEBIVENGAEMEBREMREMRPTPKESETDQALVSSVEDIL 304

Qy 271 STSKPKSPST-----PSP-----VLRKPNASQSLIUVWCKEVTKYRGKVTNFITS 316
Db 305 STCLTPNLVEMESOBAPGPAVEDVGRILSDTESWMSPLAWB-----KGNTISVMLEN 358

Qy 317 WRNGLSP-----CAILHIFRPDLIDYKSLNPDIKEUNKKAVDGAFASIG 360
Db 359 LRDSSLSLPSMLRDAIGTTPFSTCSVGTMFTPSA-----PDKSTWTSQT---GLV 407

Qy 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHFSQELANVQFENNSKSTYKVGNYEIT 420
Db 408 TKISTSETEHQLGCRGPDTALS-----RH-----DLNDNL-----L 439

Qy 421 NSSVDEQKEYAEISLDLKRPPELQOPISGAQDVDFLSDQDSVFNDSGVGESESHTPDDH 480
Db 440 SLVIVERFLSRQLRDWKSOLAVHP-----ETQDSSQTDTSHSGTINKLUHLKESH- 491

Qy 492 -----EMGQALAA-----RNWQSWVLSKIRL--SIL 518

Query Match 3.3%; Score 182; DB 6; Length 1384;
Best Local Similarity 21.1%; Pred. No. 9.1e-05; Matches 206; Conservative 115; Mismatches 346; Indels 310; Gaps 42;

Qy 493 -----EMGQALAA-----RNWQSWVLSKIRL--SIL 518

Db 519 HSILHLBEDKTTWNQSRRRASTLVCCLFDLKLKRAKLOSL---KAERHARHREMA 574

Qy 590 CR-SDPESPPIKTSLSLSPSKLGSYSRDL-----DLAKKHASLQT 630

Db 575 LRGKDAEATVLEAPCAHSQRIQSOLQDQLASRBFPGILKDMOTQVLGILHAQBLVQQT 634
Qy 631 ESPDADPDTTNEADHSSKIVQH---RILSROBLERGRARVYLEQ---RDAALKAGNK 684
Db 635 VS-----LTSFLQODWRSMOLDYTWTWALLSRSRQLATEKLYQSQAQERDVAE-EK 687

Qy 685 HNTNTATPCNRQI-----SDQODEERROLERAROLIAEARSGWYMSLPSYGENMA 738
Db 688 QEVSRVLQVSAGLCECIGTQELENLIRLANDLRAQOLQILANMDSQKELQSOQHCTA 747

Qy 739 EKUKERSKASGDENDNITDNTWBEIPECFVVGG-----GDBELTNBNDLDP 786
Db 748 QDLAMKDISLCOITQSNEQAAOCVKEEMALKHMQAEIQQQAVLAKEVRDJKETSEAD 807

Qy 787 QNSKL-----VDLKLUKLEVQPOVANSPPSAQAKVTESSEQDMSGSTDRLTRRLQ 839

Db 808 QENOVAHILGLGOVECQLKITLEVLRB--RSLOCENLKTIVENLTAKLUSTIADNQEGDPL 865

Qy 840 KITERFRPVWVKSDSTRKTQLOQSPSYIENRPEMKQRSIQBDTIGKNEGKAATETQ 899

Db 856 KTRO-----VSQKLGLITEOLOSLTUFLOTK-----LGEKTEOBTLISTA 906

Qy 900 RKPSDEBVNLKGPKDTSQYVSELAALENQ-----KQIDR-AALVEKRLRY 946

Db 907 CPPTOEHIL---PNDRFLPLGSITAVADEERESTPFLPLGDSKAFTRVAKSVLO-- 959

Qy 947 LMDTGRNTEBBERAMQEWPMFLVNUKNAILRMNOLSLRKEDLERREYLAR--ELRA 1003

Db 960 ---PAETPGMBESLAENSIMTTELQSL-----CSLQESK---EARTLQKICBLQA 1007

Qy 1004 MLAXEDQKTEQKRE-----QUL-----DELVALVNRKDALVRDQDAQK-QA 1048

Db 1008 RLQNEBQHOVOKAKEDIEKUNQALCILRYKNEKBLQEOVIOQNKEKIEQIDKSGELISL 1067

Qy 1049 EBBUHLERTLBONKGKAKGEGKCVLQ 1076

Db 1068 REFWTHURSL---RRAETEIK-VLQ 1089

RESULT 9
US-10-05-928-799
; Sequence 799, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 799
; LENGTH: 1384
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-799

Query Match 3.3%; Score 182; DB 6; Length 1384;
Best Local Similarity 21.1%; Pred. No. 9.1e-05; Matches 206; Conservative 115; Mismatches 346; Indels 310; Gaps 42;

Qy 162 PQLNPDEPEAVTIKDSPOSTKRKNIPUDMSKLYADSSKTREEELBSNPYEPK 221
Db 161 PPSPSPVRAESELSVNGHNTPTQTRGSS--ACASHSSLVSIKEQIMDSLVTBPG 217

Qy 222 STPPPNVLNVNQVOBLETERRVKRKAPAPPVLSPKTGVLMENTVSAGKD-STSPKSPPIP 280
Db 218 AGKPKPATPLSPMANGRY-----LISRPT---SPGAMSVOSSYENTSPAPSPLS 266

Qy 281 SPV-----LGRKENASOSLLWCKEVTKYRGKVTNFTTSWRNGLJSFCATLHFP 330

PRIOR APPLICATION NUMBER: US 10/1325, 899
 PRIORITY FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 3117
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2397
 LENGTH: 851
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-511-937-2597

Query Match 3.0%; Score 166; DB 6; Length 851;

Best Local Similarity 17.8%; Pred. No. 0.00052; Mismatches 284; Indels 252; Gaps 34; Matches 148; Conservative 146; MisMatches 284; Del 252; Gap 34;

QY 403 ENSSSKSTYKVGNYNTDNTSSVDPQKFYASLSDLKREPFLQQPISGAUDPLSQDSDSFTN 462

Db 84 BDSKALSKKKKKKKKKHOTKCKBIDSKNLVEKCKETK-----AN 121

QY 463 DSGVQESERSEHQTP-DDHLSFSTASPYCRR-KTKSDTEPOQKSQQSGRTSGSDP-GICNT 520

Db 122 HKG-----BENKTDLNNSIGTKKMTCSEKIDSNISPKKKSKBTQNKRKRNIVQHT 176

QY 521 DSTQAOVQLGKRLIKABTEFLSLDLVSDKCKDMSPPFICEETD-----OKLQTLDI- 573

Db 177 TDSS---LERKQRTLDGTSIEIV-----KSPRIECKTRREMQSVQLIMTRSD 223

QY 574 -----GSMLKEKLU-ENRSSL-ECRSPDPSPRIKTSISPTSKLGYSVSRLDLAKKH 624

Db 224 GYENSTDGEWCOKDALEEDSBSEVSEKGSDBESENBNITSVCGA-----SGDDGSEDE 276

QY 625 ASLROTESPPADRTILNHADHSSKITVQHR---LRSQBEELKERAVRLUORRDAALKAG 682

Db 277 BEPDDEBEBEDBEDDDKSDSGPDLARGKNIETSSBBDTADLPFSEGFHAWREL 336

QY 683 NKHNNTATPFCNRQLSDQODBERRQL-----RERAKOLIA----EARSGVMSL 730

Db 337 DKD-----APRADEITRLLAVCNDMDWLKAKDILAFNSPKRGGVIFSVK 383

QY 731 PSYGEMAEKLKERSKASGDENDNFIDTMERBEPGFWVGGBELTNLEN----- 780

Db 384 YPSFGKGKMEKEBVQVQGPVELLIS-----EDAPB-----KOWTSRKURDYQFKRLK 432

QY 781 -----DLPTRBQNSKL-----VDIQL-----KKLLEVQPOVAN 808

Db 433 YYAVVDCOSPEFASKIYBDDGLEPESCSFPIDRFIDDITEDDEPKDVAVSNLTAV 492

QY 809 SPSSAAQAKAVTRESSQDMKGSTEGLRQKTERFRNPVFVFSKQDSTVTKTQLOFSFOY 868

Db 493 KPKVFTSAAMGTSTVEITWDIDH--ERITMLARKKCFEELLDMD-----POAY 539

QY 869 I----ENRPEMKR-----SIOPDTK-----KNERCAA-----ITETOKPSD 905

Db 540 LASSEDEDEBEEBLQGDDGCVNVERDGKTKKQSQDDEOIAKYKOLLOYIOKEKKGKEN 599

QY 906 BVLINK-----GPKTSQVYVGLAALNEOKQIDTRAALVERKLRYMTGNTNTEREAM 960

Db 600 DMEMEIKWYEGLKESAREMKN-----KLEGDKLTPTEQFLKKEKRLRKKALAREAS 657

QY 961 MQE-----MLVANKNALLTRMMQNLSSLEKIKEDLERYVLLERLAM 1004

Db 658 BBLPSDVLNDPYFAEVQKQGINKKS--VKSAGKGTSPPEE-BIERO---KAEMALL 711

QY 1005 LATED-----WOKTBAQKRBQBLQJLDEBLALVN----- 1032

Db 712 WMDBEDSKKHFNPYNKVIYEHQNLISKKKKKLMIKKKLLIEDFEVNVNDARFQAMTSHP 771

QY 1033 -----KRDALVUDJDAQKOBABEDEHLERTBLEQMGKMAKKEK 1072

Db 772 NLDRSPDPNPKCTKAMEKILBKARCRERKEBLTOAIKKESBIEKESOR 821

Sequence 346, Application US/10196749
 Publication No. US200600948641
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Matanabe, Colin K.
 APPLICANT: Wood, William T.

APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEAR

TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C140
 CURRENT APPLICATION NUMBER: US10/196,749

CURRENT FILING DATE: 2002-07-16
 PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544

US-10-196-749-346

Query Match 3.0%; Score 164.5; DB 6; Length 671;

Best Local Similarity 22.0%; Pred. No. 0.00047; Mismatches 260; Indels 151; Gaps 31; Matches 145; Conservative 102; MisMatches 260; Del 151; Gap 31;

QY 465 GVGGSEBSHOTPDDHLSFSTASPYCRR-KTKSDTEPOQKSQQSGRTSGSDP-GIC----- 517

Db 76 GFNEGLWKTQ-NPHASISAPPY-----SSSDSEPARADGSDADEDDEGRYMAVTA 131

QY 518 -----SNTDSTQAOVQLGKRLIKABTEFLSLDLVSDKCKDMSPPFICEETDOK 567

Db 132 TATAASDRMESSDSDDSKDSDNSGLK-----KTPALKNS-----VSKRARKAS-----SDLQAS 181

QY 568 LOTIDIGSMLEKLEKLNRSLESRDP-----SPIKTSLPLTSK-----LGYSYSDJLAKGH 624

Db 182 V-----SPSEBEESESSSESEKTSDFDTPBKAVAPRGRPLG-----GRKKCA 228

QY 625 ASLROTESPPAD-----RTLWADHSSKITVORHLRQEELKERAVLLEQAR 674

Db 229 PSASDSDSKDCAKPRVAMARSASSSSSSSSSSDSDVSKPRKPKPLPKP 288

QY 675 RDAALKAGKHNNTATPFCNRQLSD-----QODEERRQQLERAROLIAEKS 723

Db 289 -----GKPKP-----RPPSSSSDSDSBDVSEMRDEARRELRARRRQE----- 337

QY 724 GVKMSLPSYGYEMAEKLKERSKASGDENDNLTIDTNHPIPGFVVGDELNTLNLID 783

RESULT 13

US-10-196-749-346

RESULT 14
 Db 338 ----ELRLREQEKEK-KERRRERADRG-----EARSGGGSGDEUR--EDDEP 380
 Qy 784 TPEONSKLVDLKLKULLLEVQP--QWANSPPSSAQAKAVTSSBODMSKGSTDPLTRLOKT 841
 Db 381 VKKGRGKGRRGGPSSSDSEPBABLEREAKKSAAKPOSSTREPARKPGQKEREVRPEBKQ 440
 Qy 842 TERPRNPVPUFVKSTOVTYKQLOQPSQYIENRPEMKRQSIQDUTKKGHE-KAITEQR 900
 Db 441 Q-----AKPVKEVERTRIKRSBGPSSMDRKVEKKEPKSVEKLUQKHSIEKIPALKUD- 489
 Qy 901 KRSDEDEVNKGKFDTSQYVUGELAILE---OKQIDTRALVEKRLYLMGTGRNTE 956
 Db 490 SPDVKRCAN-----ALEBLGTLQVTSQIQLQNTDVATL-KIRRYKAMKDWEKA 539
 Qy 957 EAMMQEWMLVNKNALJRRMNOOLSLIKEKENDLERYELLNRBLRAMLAIBDWQKTA- 1015
 Db 540 AEVYTRLKSRLVGPKIAEVQVKVKAG-MEKEKAEK-----LAGBLVLAGEBAP 586
 Qy 1016 QKEREQOLLDDELVALVNTERDALVRDLDAQEKKQAFEEDEHLERLTLEQNGKMKARKEKC 1073
 Db 587 QEKAKEDKPBSTDLSAPVN-----GEATSQKGESAEDKEHEE-----GRDSBEGPRC 631

RESULT 14
 US-11-252-276-22
 ; Sequence 22, Application US/11252276
 ; Publication No. US20060094868A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Bright, Gary
 ; APPLICANT: Olson, Keith
 ; APPLICANT: Burroughs-Fenca, Sarah
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-R2-CO
 ; CURRENT APPLICATION NUMBER: US/11/252,276
 ; CURRENT FILING DATE: 2005-10-17
 ; PRIOR APPLICATION NUMBER: 09/713,572
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: 09/430,656
 ; PRIOR APPLICATION NUMBER: 09/398,965
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 09/031,271
 ; PRIOR FILING DATE: 1998-02-27
 ; PRIOR APPLICATION NUMBER: 08/810,983
 ; PRIOR FILING DATE: 1997-02-27
 ; PRIOR APPLICATION NUMBER: 60/136,078
 ; PRIOR FILING DATE: 1999-05-26
 ; PRIOR APPLICATION NUMBER: 60/106,308
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 168
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 1610
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Description of Artificial Sequence:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; US-11-252-276-22

RESULT 15
 US-10-511-937-2566
 ; Sequence 2566, Application US/10511937
 ; Publication No. US20060088836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
 ; APPLICANT: Wohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodard, Robert
 ; APPLICANT: Ly, Ngoc
 ; APPLICANT: Prentiss, James
 ; APPLICANT: Morris, MacDonald

APPLICANT: Rosenberg, Steven
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
 TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
 FILE REFERENCE: 50661200104
 CURRENT APPLICATION NUMBER: US/10/511,937
 CURRENT FILING DATE: 2004-10-19
 PRIOR APPLICATION NUMBER: PCT/US2003/012946
 PRIOR FILING DATE: 2003-04-24
 PRIOR APPLICATION NUMBER: US 10/131,831
 PRIOR FILING DATE: 2002-04-24
 PRIOR APPLICATION NUMBER: US 10/325,899
 PRIOR FILING DATE: 2002-12-20
 NUMBER OF SEQ ID NOS: 3117
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 2566
 LENGTH: 1186
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-511-937-2566

Query Match 3.0%; Score 162.5; DB 6; Length 1186;

Best Local Similarity 18.4%; Pred. No. 0.0015; Mismatches 417; Indels 395; Gaps 53; Matches 221; Conservative 167; Mismatches 417; Indels 395; Gaps 53;

Qy 2 KQYASPMPTODVKUKPKPSKKVVAHSALOFLSLCIFLRREGKATDEDMQSIALSLVSMKOA 61
 Db 95 KDLASSRKRTEKULKTPLKQTAFR-----SKDEALSLITQ--RREN 141
 Qy 62 DIGNLDDPERD---NEDDDE---NRVNQDEBKAAKITELINKUNFLDBAEKDLATVN 113
 Db 142 DLYVAPPLQBEKHSSBEEDEKEWOMNO---KOALQESFFHNPDAIDIESDFSSL--- 196
 114 PFDPPDAEILNPGDPSBRITB-----TASPRKTED----- 146
 Db 197 --PPEV-----KHLITDMKEFTKRRTLFTEAMPEBESDFSQYQLKGGLKKNYL 243
 Qy 147 -----SFYNNSYNPFKEVQTPQYLNPFDEPAFTVKIDSPPOSTK 186
 Db 244 NOHTEHVQKEMNQHQHSQHTTRQYEDEGEFLKEVSSRRVS--EDPSHYTLKGQAKTV 301
 Qy 187 RKNTRPVDMKRYLYADSSKTBEEELDESNPYPYEPKSTPP--PNVQEL 236
 Db 302 EVDSELSPSSSKMKGMSFDVUSSPCKEKLKTKKEPDATPSPRTLLAMOALLGSSBEEI 361
 Qy 237 ETEREVK--RKAPA-----PVLSPKPGVLMEN---TYSACKDLSTS PKSPKSP 282
 Db 362 ESENKRQARGRGNAPAVDEGSISPRNTLSA KRALDDDEDVYKVACGDVORG----- 412
 Qy 283 VLGKRNKASOSLLVWCKEVTKNY-RGVKLTNFTSWRNGLSFCATLHFRPDLDYKSLN 341
 Db 413 ---GPGAEEMRI--NSSPENDEGLKVRD---GKJGPPTATLAS-----SSYN 452
 Qy 342 PQDIKENNKCKAYDGFASTGISRLIPSDMWYLATAIDPKLTWTLYQIRAHFFSGOBINWQ 401
 Db 453 -----SPEERVASTNEGR--SPTDSV-----PKGOMSLVH 480
 Qy 402 IEESSSKSTVKGNTVETDTNISDVQDKPYVLSLDRBLQQPIGSAVDPFLSODDSVRF 461
 Db 481 -----VGTAEF--P-IDS-----ESMKDRKDRPLSAVR 509
 Qy 462 NDSGVGSESEHQIPDDHLSFESTASPYCRTKSDFTEPOKSQSSORTGSSDDPGICNSID 521
 Db 510 HSDAGGLPNRBLTP-----ASPTCTMSVSK----- 537
 Qy 522 STOAOVTLGKRRKLKABTLSLSDVSKDKDMSPPPICHTBOKLQTIDIGSNLEK 581
 Db 538 -THARVLEQOBMLCYTESKFDSLSSSDATCKCDNSASEFVIGPVSLQSTTSIVVPSEA 596
 Qy 582 LENSRSLECRSSDPBSPIKITSLSPIGGSYSRDLAKRKHASLQTESPPADRTL 641
 Db 597 VDNVENV-----VSFNAKHENFLETIOEQQTESAG 628
 642 NHADHSSKIVQHRLSLRSQEBSKERARVILLEQARRDAALKAGNKINTATPPFCNRQLSDQ 701

Search completed: May 20, 2006, 17:30:35
 Job time : 18 secs

Db 629 QDLTSIPKAVEPMEIDESSESSESDSGSPFEVSVISDEELQ-----SPPETSKPSEQ 680
 Qy 702 QDEERRRQLRERAROLIAEARSGVVKMSLPSYGENMAKURKSKASGDENDNIRIDNE 761
 Db 681 GEER-----LV-----GTRGRAPAESSSLRNRNSERODVDG-SPORAKDAED 723
 Db 762 BIEGFVUGGGDELNTNLENDLDPBONSKULVDLKUKK-----LLSVO---- 803
 Qy 724 SLHEWQDI-NLEELTLESLN-LAQONS---LKAQKOOBRIAATVTCOMPLSQUELL 777
 Qy 804 ----POVANSPSSIAQAKATESSRSODMKGSTEDEARTERLOKTTFRNPVVFSTURK 859
 Qy 812 -----SPPVQVYDQHDFHOLGRNKLINLAYLVLGSDYTEGIPWGVCTAM-----BILNRP 881
 Db 778 LFGIPYIQAUMEAEQACIATLTDTSQITDD-SDMILWFGARAVYRN--PFNDKPFV-- 832
 Db 860 TQLQFSRQYR--NREPMEKQRORSQ----EDTKKGNERKAITETORQPSDEVINK- 910
 Qy 833 -----EYVQYDFFHNFHOLGRNKLINLAYLVLGSDYTEGIPWGVCTAM-----BILNRP 881
 Qy 911 ---GFKDTSOYVVBALALENEQKOIDTRALVERKRYMDTG--RNTBEEAMMQENF 965
 Db 882 PGHGLPPLKESEWWHEAQKNPKTRPNPDTKVKKRLQLTCPFPNPVAEAYLP-- 939
 Qy 956 MLVNUKNAIJRMQMLSLRKEHDLERFELLERBLRAMLAIEWQKTAQREHQLLJD 1025
 Db 940 -VVDISKG-----SELWKGPKDIDKTRFCQRYF-----GMNR-----KTDLSF-- 978
 Qy 1026 ELVALVNKRUDALVRDQDKEQ-----ABEDDEHILERTLBONKGK--MAKKEK 1072
 Db 979 -----PVKQDLDQATQRLIDSFRLAQKEDKRIKSORLNAVTCLMRKE 1028

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QV	310 INTNTTSWRNLSLFCALIHHFRPDLI-DYKSLNPODIKENN-----KKAVPQFASIGI	361
Db	353 VNDFTKSWNGLALCAVLHSYRPDLIGDYL---DISNMGRISNIORALDSLTLGI	409
QV	362 SRLLEPS-DMVLAIAPDKLTWMTLYQIRAHFSQELNVYIERNNSSTYKVGYEFT	420
Db	410 TEV--PTVDMFL--TPDRKQIEFLQHQLRIFEG-----FDGEGSPASDRISRTF	458
QV	421 NSSVDPQEKEYAELSLKRPPELLOOPISAGAVDLSQDDSVFVNDSGVGESESEHOTPDHL	480
Db	459 GINESEEKVAMITTEIRNOLES---AVDYRHPDEPV-----	495
QV	541 ELDLYVSDKKKOMSPPFICEBOKLOLTDIGSNLEKEKLENRSRBCRSPESPTRK	600
Db	520 - -----SNMRPER-----SNVSI	531
QV	601 TSLSPSKLGYSYSLDOLAKKHASLROTESUPDADRTLNHDHSSKIVQHRLLSQE	660
Db	496 TPQLAS---RNPLNQP---TDAIDD-----DART-	519
QV	532 TWMTP---GVGAIR-----ASNRP-----	533
Db	532 TWMTP---GVGAIR-----ASNRP-----	533
QV	661 ELGERARVILLEQARRDAALKAGNIGNNTATPFENRQLSDQOBERRQLRQLTAE	720
Db	554 ELQRAROLIE-----XSTPRAATPNRK---ASDERR--REVRMLNE	594
QV	721 ---ARSGVKSMBELPSYC-----	757
Db	595 KQHPTAIRSTSSSPYPTFRIDSNTDLRILBLDVHKPKRDPSPTLVRQVQPDNT---	651
QV	758 DTNEEIPSGFVGFGDELTLNLENDLDPFQNLSKVLKLUKLLVEQPVANSSSAOKA	817
Db	652 ---PRVPAIGRGTNCN-RND-----	676
QV	818 VTESSEBQMKSGIEDLTERLKUTTERPNPVFSKDSVTVKTQLOFSQYIENRPMKR	877
Db	677 ---TDFRK-----RYGSMRASBLK---ESLQLMAK	701
QV	878 QRSIQEDTKKGNEKAITETORPKPSEBVLNKQPKDTSQYVGBLALENBOKQIMRA	937
Db	702 QYGMGMNDPESSODALATPTKRESSOWB---KD---VDDVEGTANELVRIDERI	750
QV	938 ALVEKRLYLMPGCRNTS---IREAMQEWMLVNUKVALIRRQMQSLLEGHDLERR	993
Db	751 SDTTAQADVYDQKIRETEVGSSBMLTASYLNTNERLTVRQBYNTIETRQTF	910
QV	994 YELLNLRELRAMLAEDWQTEAQKREQOLLDLVALVNRDVALVRLDQAEQKAEDE	1053
Db	811 IDLGKQNEV--PDPEFRSDENKTATDKLICQSYDAMKTKSNLVQKLFATEDEIEBSD	868
QV	1054 HIZR-TLEQ 1061	
Db	869 RKLNTLDR 877	
RESULT 2		
T14867	interactin - slime mold (<i>Dictyostelium discoideum</i>)	
C;Species: Dictyostelium discoideum		
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004		
C;Accession: T14867		
R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.		
J. Cell Biol. 142, 735-750, 1998		
A;Title: Interactin, an actin-binding protein of the alpha-actinin superfamily in Dicty		
A;Reference number: 218248; MUID: 98365468; PMID: 9700162		
A;Accession: T14867		
A;Status: preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type: DNA		
A;Residues: 1-1738 <RIV>		

Qy 1051 EDERLERTERQNKGMQAKREK 1072
Db 1014 LQSOLNEQRQQNQNLSEKDQ 1035

RESULT 3

S28381 urophin - human
N: Alternative names: dystrophin-related protein.
C: Species: Homo sapiens (man)
C: Date: 17-Apr-1993 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C: Accession: S28381; S28914; S03966
R: Tinsley, J.M.
submitted to the EMBL Data Library, November 1992

A: Reference number: S28381

A: Molecule type: mRNA
A: Residues: 1-2943 <TM>
A: Cross-references: UNIPROT:P46339; UNIPARC:UPI00013786A; EMBL:X65086; NID:934811; PIDN:R7TINSLEY, J.M.; Blake, D.J.; Roche, A.; Fairbrother, U.; Riss, J.; Byth, B.C.; Knight, Nature 360, 591-593, 1992

A: Title: Primary structure of dystrophin-related protein.

A: Reference number: S28914; MUID:9306045; PMID:1461283

A: Accession: S28914
A: Molecule type: mRNA
A: Residues: 2944-3435 <LOV>
A: Cross-references: UNIPARC:UPI000000673; EMBL:X15408; NID:930933; PIDN:CAA33515_1; PID:503966
A: Molecule type: mRNA
A: Accession: S03966

C: Comment: This protein is found primarily at the neuromuscular junctions in adult muscle regenerating muscle.

C: Genetics:

A: Gene: GDB:UTRN; DMDL

A: Cross-references: GDB:119851; OMIM:128240

A: Map position: 6q24-6q24
C: Superfamily: dystrophin; alpha-actinin actin-binding domain homology: spectrin/dystrophin binding; cytoskeleton; leucine zipper; membrane-associated protein; microtubule-associated protein

C: Keywords: actin binding; cytoskeleton; leucine zipper; membrane-associated protein; microtubule-associated protein; spectrin/dystrophin repeat homology <ACT>

F: 308-417/Domain: alpha-actinin actin-binding domain homology <SP01>
F: 418-526/Domain: spectrin/dystrophin repeat homology <SP02>
F: 528-637/Domain: spectrin/dystrophin repeat homology <SP03>
F: 638-885/Region: hinge
F: 686-796/Domain: spectrin/dystrophin repeat homology <SP04>
F: 804-902/Domain: spectrin/dystrophin repeat homology <SP05>
F: 906-1013/Domain: spectrin/dystrophin repeat homology <SP06>
F: 1015-1121/Domain: spectrin/dystrophin repeat homology <SP07>
F: 1124-1230/Domain: spectrin/dystrophin repeat homology <SP08>
F: 1233-1334/Domain: spectrin/dystrophin repeat homology <SP09>
F: 1339-1450/Domain: spectrin/dystrophin repeat homology <SP10>
F: 1451-1541/Domain: spectrin/dystrophin repeat homology #status atypical <SP11>
F: 1543-1649/Domain: spectrin/dystrophin repeat homology <SP12>
F: 1651-1755/Domain: spectrin/dystrophin repeat homology <SP13>
F: 1856-1973/Domain: spectrin/dystrophin repeat homology <SP14>
F: 1975-2081/Domain: spectrin/dystrophin repeat homology <SP15>
F: 2083-2185/Domain: spectrin/dystrophin repeat homology #status atypical <SP16>
F: 2222-2333/Domain: spectrin/dystrophin repeat homology <SP17>
F: 2335-2440/Domain: spectrin/dystrophin repeat homology <SP18>
F: 2442-2556/Domain: spectrin/dystrophin repeat homology <SP19>
F: 2558-2688/Domain: spectrin/dystrophin repeat homology <SP20>
F: 2699-2797/Domain: spectrin/dystrophin repeat homology <SP21>
F: 2798-2869/Region: hinge
F: 2812-2849/Domain: WW repeat homology <WW1>
F: 2837-3117/Region: cysteine-rich
F: 3263-3284/Region: leucine zipper motif
F: 3328-3349/Region: leucine zipper motif

Query Match 5.9%; Score 326.5; DB 1; Length 3433;

Best local Similarity 19.8%; Pred. No. 6.4e-06; Indels 303; Gaps 37; Matches 197; Conservative 159; Mismatches 336;

Qy 285 RKPNAQSILWCKEVTNYGRVKTINFTISWNLSTCALLHFRPFLDYLKSINPRPDI 345
Db 148 QQTNESEKILISWWRQTTTFSQTNLNTMSWTDGLATNAVHLRKPLPSWOKVKVNSP 207

Qy 346 KENNKKAVGFPAS-IGSRLLERSDMVLIAIPDKLTWVTLYQI----- 388
Db 208 IERLEHAFSKAQTVLGITKLSDRD-VAVRLPKKSITIMYLISLFEVNPQQVTDIREV 266

Qy 389 ---RAHFGQELNVVQFRENSSKSTYKVGYETD--TNSSYDQEKKYAEELSDLKRPE 441
Db 267 ETLPKYKKGCEBAINIQSTAPBEHRSRPAETPSTTEVDMDLSYQIALEV---- 321

Qy 442 LQPPISGAVDFLSCQDSDTFVNDGGESSESHOPTDPLSPASP-----Y 488
Db 378 TQGFLSDRPEREFOQWNTLNARWEALRVESMORSRHD-VLMELQKQKQLQLSAMIT 435

Qy 529 LGKERRLLKAKTBLSD-----LYVSDKKKOMSP 556

Db 436 LTBERIQKMETCPFLDDWYKSLQKJLEHHSKLSQDLEARQVKVNLTHAVVIDENSGSA 495

Qy 557 PFT-----CEETBQ- IQLTDIGSNKEKLENSSLECRSDPESIK 559

Db 496 TAILEDQLOGLGERWTAVCRWTERWNHLLFEE---OCLIKAWLTK 548

Qy 600 KTSISPTSKGYSYSDIDLAKKKHASTQTESDPADRTTINAHDSKIV----- 652

Db 549 BEALNKVQTSNFQDKERSVSVRALIKE--DMEMRQTL--DQSBIGDVQQLD 602

Qy 653 ----HRUJSRQEHLKER-----AVTLLSQR-RUA 678

Db 603 NSKASKKINNSDSBLLTQWLDLSSNQVTOAVKUGMSQIPQCDLLETWVRVQA 662

Qy 679 LKAGNKHINTATPPCNQQLSDQDERRQLRERARL-----IAEARSGVKMSELSPGE 735

Db 721 MDTSEMKGKLKA-----LEQEOREIPR-----ABELNQGQJVBQMKGEGLPTE 767

Qy 653 ITKSKQKSLPPPQPKQI-HVDIBAKKFDAISALANLNWKWKAQIT'VEKTMK 720

Db 736 MA-AEKLAERKSKASGDEMDNIEILDNETPEGFVGCGDQLTLNLDIDTPPEONSKLVLD 794

Qy 775 KLUKULFETOPQVANSPPSAQKAVTTESSBDMKSGTEDLIRTERLQKTERFRNPUVFKD 854

Db 768 EIKNVLB-----KVSSEWKNVSQHLDLERK-----IQLOED 799

Qy 855 STTRKTOQFSQYIENRPEMKRQSQDFT-----KGHEEK 892

Db 800 INAYFKQDQJDELEYKTKTBEWKGTSISESSRSRSLPSLSDSCORELTNLGJPKIENR 859

Qy 893 AATTETQRKPSDEDEVNGCF-----KDTQSYVVGELAALNEQKQIDTRA 938

Db 860 ASCSALMVOQPSADFVQGFDSTFLGRYQVQVAEVEDROQH-----LENELKGQGPGRAY 912

Qy 939 LVERKLRYLMLDTRNTR-----FREEMNOEWFLVNUNKONALTRM 978

Db 913 L-EETLKTKDVKLNDSEKRAQSVLNLVNDLAKVETKALQKKTLE--TLENOKPALKLCA 968

Qy 979 NOISLKEE-EHDLRVEELLERLRAALAEWQKTAQKRRQQLLDELV----- 1028

Db 969 EETKALEKKNHPDVKLQKEDVQG-----KNNKAVLVLSDHLHFEALTLRAREA 1023

Qy 1029 --ALVNKGDALVDDQABQKABEEDLERTLEQ 1061

Db 1024 DSTVIKMDGVKDFLMMQQAQGDDAGLQLDQ 1058

RESULT 4

T34419 hypothetical protein F12F3.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T34418
 R;Fuller, B.; Wohldmann, P.
 submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of *C. elegans* cosmid F12F3.
 A;Reference number: Z21521
 A;Accession: T34418
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-3188 <FULL>
 A;Cross-references: UNIPARC:UPI000017B8E6; EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023;
 A;Experimental source: strain Bristol N2; clone F12F3
 C;Genetics:
 A;Gene: CESP:F12F3.3
 A;Map position: 5
 A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
 Query Match 5.9%; Score 324.5; DB 2; Length 3488;
 Best Local Similarity 19.1%; Pred. No. 8a-06; Mismatches 429; Indels 397; Gap 54;
 Matches 245; Conservative 215; Mismatched 429; Indels 397; Gaps 54;
 Qy 25 VISAALQPSLSCIFLRESKATDPMQSLASLUSMVKQADIGNDD--FEEEDD-DENR 80
 315 VAGEBAWCPSDVVMHSE-ESRD--D----KSVDEVDTVLEKKDKGDKSK 361
 Qy 81 VMEBEKAAKTIEELINKUNFLDAEKDLATVNNSNPFDDDAEELNPFGDPDSEPIETAS 140
 362 PRKTKKKLIIKKG-TPEBSQVTAAPPEQOKIISVUDQSVAETSGAKCKPDAKP-TDSLK 419
 Qy 141 PRKTEDSPYNNSYNPFPKEVOTPQYLNPFDEPAFVTID--S-PROSTKRKNR 191
 420 AKKDSKS-----KVSDEPASTEERKSTTRKPTNDKTISKSAEKKIV 461
 Qy 192 PVDMSKVLYADSKSTEERELDSNPFPKSPSPPPNNLNUVPOBLETERRYVRGKAP--- 247
 462 PKKEVTKSPLKPKLAKPKVSDKDKAQSPSSKESPP-----TDGKKHQIPALF 509
 Db 510 IPDELISSRFG-----DPSMTMSEINTNTITRGREGSSADAKPVL--EPISAVY 555
 Qy 307 GVKITNFTTSWANGLSFCATILHHRPD-----LIDYKSHNPQD-----IKE 347
 Db 556 SMKVFTLVESAKEKAESPKRSRSETPDPSKRKEGLPPAKESKEKKDDEVTABQSTEALIE 615
 Qy 348 NNIKKAVDGFAIGISRLR--PSD--MULLAIPDKLTWMTLYQIRAHFSQEL--NNV 400
 616 SKRKEVDE-----SKIEQQSDKNSKEWVWPEKA-----AGPETKKDV 656
 Qy 401 QBIENNSKSTKTYGVNEYDTTNSVQDKFAYLSDLKREPELQQPISGAVDPLQDSVF 460
 657 EIEEVPKKTTKTKTEKD--S-SIQSQNSVNPAD-----ddksksdvv- 698
 Db 461 VNDSGVGESSEBHQTPDHLSSTASPYCRRRTSDTPEQKQGOSSGRTGSDDPGICNT 520
 Db 699 -----TDKSKKTTEDQTKWAD-----KLEKAADTTQIETVVDK----- 737
 Qy 521 DSTOAGVTLGKRRKLKATLSDLVSKDKKDMSPPI---CESTDQEQKLTL----- 571
 738 -----SKKVKVKKT-EKSDSFISQKS--TPPVVEPTPKPARSEAOKIAEVNACK 785
 Qy 572 --DIGSNLEKEKLENSRL--ECSRDPESITKTSIULPTSKLGYSYSDLDLAKKKHAS 626
 Db 786 QKEVDNLKREAEVAAKTIAEAKLKEEAANIKKA-----EVAAKKQKEK 832
 Db 627 LROTESDPD-----ADRTTINHADHSKTVVOHLISROEELKERRVILLEQARDDA- 678
 Db 833 DEQLKLETEVVSKSAEAKLEQAOQIKKAAEADAVKKQELNEKNK--LEAAKSAAD 890
 Qy 679 -----LKAGNKHNTNTATPFNCNQI-----SDQQDE 704

RESULT 5
 PDBAA
 alpha-actinin - slime mold (*Dictyostelium discoideum*)
 C;Species: *Dictyostelium discoideum*
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C;Accession: S00103; 29006
 R/Noegel, A.; Witke, W.; Schleicher, M.
 FEBs Lett. 221, 391-396, 1987
 A;Title: Calcium-activated non-muscle alpha-actinin contains EF-hand structures and high
 A;Reference number: S00103; MUID:87304850; PMID:3622778
 A;Molecule type: mRNA
 A;Residues: 1-362 <NOE>
 A;Cross-references: UNIPROT:PO5095; UNIPARC:UPI0000125099; EMBL:Y00699; NID:9717; PIDN:
 R/Witte, W.; Schleicher, M.; Lotzspeich, F.; Noegel, A.
 J. Cell Biol. 103, 969-975, 1986
 A;Title: Studies on the transcription, translation, and structure of alpha-actinin in Dic
 A;Reference number: A29006; MUID:66304574; PMID:3745276
 A;Accession: A29006
 A;Molecule type: DNA
 A;Residues: 92-359, 'P', 361-500, 'T', 502-505 <WIT>
 A;Cross-references: UNIPARC:UPI000016B8E8; EMBL:X04324; NID:97202; PIDN:CMA27855.1; PID:
 C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin rel
 C;Keywords: actin binding; calcium binding; duplication; EF hand; homodimer
 F;21-236/Domain: alpha-actinin actin-binding domain homology <ACT>
 F;266-377/Domain: spectrin/dystrophin repeat homology <SP1>
 F;386-493/Domain: spectrin/dystrophin repeat homology <SP2>
 F;505-607/Domain: spectrin/dystrophin repeat homology <SP3>
 F;611-717/Domain: spectrin/dystrophin repeat homology <SP4>
 F;730-762/Domain: calmodulin repeat homology <EF1>
 F;766-798/Domain: calmodulin repeat homology <EF2>
 Query Match 5.8%; Score 321; DB 1; Length 862;

	Best Local Similarity	23.3%	Pred.	No.	1-9e-06;	
Matches	187;	Conservative	96;	Mismatches	262;	
Indels	256;	Gaps	35;			
b	2.89	NASOSILVWCKEVTKNTYRGKTKINTTSWNGLSFCALMHFRPDLIDYSLNPODKIEN	348	A; Residues:	-1-2128 <RES>	
b	1.38	SAKEALLWWORKTGYDRYGNFTSFDGLAPCALIHKHRPDLINPSLNKDAGN	197	C; Cross-references:	UNIPARC:UPI0000029884; GB:566283; NID:9440899; PID:AB28600.1; PID: A; GenBank ID: Spnb-1	
b	3.49	NRKAKD-GFASIGSRLLSESDMVLIAIPIKLTWYIQLRAHSGQELNVVIBRENS	407	A; Gene:	Spnb-1	
b	1.98	LQLARFIDAKEKELDIPKMDLOVSDMLDVPRPERSWVYVYVYTHRSAS	252	A; Introns:	418/3; 1742/2	
b	4.08	KSTYKVGYNTDTMSSVDOXKPYAFLSD-LKREPLOQPIGAVDPLSODSVFVNDSGV	466	C; Superfamily:	spectrin beta chain; alpha-actinin actin-binding domain homology; spectrin	
b	5.26	--QVILGKCRLLKARTLESLDLYVSDKKMSPPIC-----BETDEQKLTDIGSNL	577	C; Keywords:	actin binding	
b	2.53	KQVGKV---LDTFMLEBQK---SDYLRKANBLQWIN-----DKQASLESROP	295	F; 53-271/Domain:	alpha-actinin actin-binding domain homology <ACT>	
b	4.67	GRS-ESRHQPPDHHSPTASPYCARTKSTPQKSQSGRTSGSDPQICNSWIDSTQA	525	F; 187/Domain:	spectrin/dystrophin repeat homology <SPH>	
b	2.96	GDSTIESVOSPMNAH-----KEYKTEKEPKPGQEV-----ELBA	329	Query Match	5.8%; Score 319; DB 2; Length 2128;	
b	3.30	IYNSLQTKURLIKOB-----		Matches	221; Conservative 160; Mismatches 382; Indels 358; Gaps 44;	
b	5.78	EKEKLENSRSLECRSDPESI-----KKTSLSPSKUGSYSIDL-DIAKKHA	625	Qy	285 GRKP-NASOSILVWCKEVTKNTYRGKTKINTTSWNGLSFCALMHFRPDLIDYSLNPO	343
b	6.26	SIRQTE-----SDPD-----ADRTTINH-----ADHSS	648	Db	169 GREQRSAKDALLWNCOMKTTAGYPHYVNTNFPSWKDGLAFNALIHKHRPDLIDFDKIKDS	228
b	4.25	KLKQNLAFDGEBCQSLEGQOONSLSLISAQIOTELNNGVPELTERTFAQWTGUKSSA	484	Qy	344 DIKENKKAYD-GFASIGSRLLSESDMVLIAIPIKLTWYIQLRAHSGQELNVVQ	401
b	6.49	KIVORHLRSRQEELKERRARVILEQARRDAAL---KAGNKR----NTWATPPCNRQ-	697	Db	229 NARHNEHAIDVAHQLGITPLDDED-VFTENIDEKSIITYVAFYHFSKMKVLAVER	287
b	4.85	ETYKNTTIALBLERLOKIEDLSIVEFAKRAAQOLNVWIEAADHVFPDPINVDVGQVBEOQK	544	Qy	402 -----IEE-----NSSK-----STY	411
b	6.98	---LSDOD-----		Db	288 KRVGVKVIDHAETEKMIEKYSGLASLDLTWIEQITISVLSRKRANSLSGVQQQLOAFSTY	347
b	5.45	FDAPLHDQSQFQABLEALAAUTOQRELGRSENDYVISDELSAKWNNLLAGIBERKVQ	604	Qy	412 KV-----GNYET-----DTNSVDOEKPTAB-----LSPIKR-----REPELQQP	445
b	7.10	LRERARQQLAEARS-----GVKOMSLSYGEMAAEKURSKASGENDN---IEID	758	Db	348 RTVEKEPKPKFQEKGHNLEVLVLIPTIQSMRANKNQKVTPHDGKLVSDINRAWESLERAEYORE	407
b	6.05	L---ANELTQTONNDVLCOSPSVKANEISDYVRTTIDASONTSSDPPQQLNNRRAITA	661	Qy	446 ISGAUDPLSODSDSFVNDSGVGB--SESEHQTDDHLSPTASPYCRRK-----SDTE	497
b	7.59	TNEBLPEGFVGFGGGBLTNLENDL-----DTPEONSKVUDLKUK---KLLVQPOVA	807	Db	408 LALRSSELIROE--FDRKAMREFTWINEQRLVYQDNFGYLAIVEAKKGHEATEDTA	464
b	6.62	HAECKPE---LDELYTTRSQLBEAQOVNDNKHTQHSLESLJKWJKWDKLTLAKKNEQV	715	Qy	498 POKSO-----QSSGRTGSDDPGICNSNTDS-----TOAQLVIGKCRLLKARTLESD	544
b	8.08	NSPSSAAQ-KAVTTESEQMKS-----GTEDLATERLQ-----KTTERFRNPV	850	Db	465 AYERVKALEDBLADBLEKENEYHDKRIIARKNDNIRLWSYLQBLRSRQRORLEATLQK	524
b	7.16	EGBTLAKOGLTGUTAELBSEPKACPSHFDKONDNLKLRFSSCLXKISGDELTERBOLNPVY	775	Qy	545 LYVS-----DKKKOMSPPFICEETDEQKLOLTDIGSNLKEKLNRSRSCRSPPESPIK	599
b	8.51	FSKDTSTVRKTOLOPSQXYENRPEMKRQKSIQEDTKGG---NIEKAATETORKPSDE	906	Db	525 LFQDMHSHIDWMDIEKAHILSAEFGKHLLEVEDL---LQHKHMEA-DIAIQGDKWKATT	580
b	7.76	SKDTRGNGT---ISPFRTDYMPSRKGDVSVESTIKAFKVMAEDKDFTBAQ-----	826	Qy	600 KTSISPTSKLGYS-----YSRQLDALKKHSALRQTES-----	632
b	9.07	VLNKGPKPSO-YWVGELAALB	927	Db	581 AATIQFAEKGKQYCDPQVQIOPDRVSHLEGQCPSELSNMANGKACLEQSKRMLWKFMEMDB	640
b	8.27	-IRAAISDSKQIDVILLASMPAVE	848	Qy	633 -----DPAADRTRNHADHSKSTVQHRLLSRQBELKE-----	664
b	9.25	7		Db	641 AESWIKERKEQIYSSIDYQGDLTSILQORKKATEDELGLDAHLKQFQBADDNVAQKQ	700
b	9.25	7		Qy	665 -----RARVLEQARD--AALKAGKMENTNTATPP-----CNRQLSD	700
b	9.25	7		Db	701 FGHPQIETRKYKEVAQWDLKELLAFKRKLQDALENFFQGDDAIIKAWLQDARILLSG	760
b	9.25	7		Qy	701 Q---QDEBRRQLRERARGQLAEARSQGVMSLELSYGENMAEKURSKASGENDNIEI	757
b	9.25	7		Db	761 EDVSGQEGATRALSKKHKEPLEEERSRGVME--HLERQAOQGPFERFDSPDVTNLQA	817
b	9.25	7		Qy	758 -----DTNEBEIGEVGGGD-----ELTNENDLDT	784
b	9.25	7		Db	818 LRKQYQVQVTAQEAERLGHKQOBALIUYTFGERSIDACELWMTBKGKWLQMDIPNTLDEBV	877
b	9.25	7		Qy	785 PEQNSKLVQVLTQAEIYRQVQVANSPSSAAQKAVTTESSRDMKGEGTEDLTERI-QKTER	844
b	9.25	7		Db	878 VQHFFDILDORMKUMLAQDGV-----NLAANNLIVESCP-----RSGEVKQYODRANKRWA	930
b	9.25	7		Qy	845 FRNPVVFSK---DSTVRK---TOLQSFQYIENRPEMKRQKSIQEDTKKGNBKAITE	897
b	9.31	904VSEQRBAVDSLARVNVYCUCBETSKWINDKTK---WVESTQDGLQDLAGVIA	984	Db	931 IQRKLSGLERDVLAIRDRVSLAERESQY---LMESHSPQEKGQROADVEKWKGLQD	1040
b	9.88	TQKPS---EDBVIN-----KGFKTQSOVYGEALLENBOKO-IDTRALVKEKLYMD	949	Qy	998 TQKPS---EDBVIN-----KGFKTQSOVYGEALLENBOKO-IDTRALVKEKLYMD	949
b	9.88	-----STATUS: preliminary; translated from GB/EMBL/DDBJ		Db	-----	

QY	950 TGRNTE-----EEAMMQE-----WFLVNKNA-----LIRMMQSLIEK 986
Db	1041 ALQQBLSLGASKLQAFQLDQDDFKAWLSMAQKAVASEDMPSIPEAEQOLQHAAIKE 1100
QY	987 EHDLER-----RVEELNRLLRAM-----L 1005
Db	1101 EIDAHRDYHRVKASGEKVGIEGGTDPDQYQGQINGLEGUDWMDARLMWESRGNTLTQCL 1160
QY	1006 AIEDWQKTRAQ-----KRREBQLI-----DELVALKNDVRLD 1041
Db	1161 GFQBFFQDKAQAEMLNSNOBYTLAHLPPDSLAAEAGIRKFEDFLVSMENNDRKILSPV 1220
QY	1042 DADRKQABERDEHLRTLE-----ONIGKMKAKKEKCVL 1075
Db	1221 DSGNKLVAEGNLYSNKIMERKVQLTDRHKNNKEAQATVL 1261
RESULT 7	
QY	transport protein USO1 - yeast (<i>Saccharomyces cerevisiae</i>)
Db	N[Alternative names: protein D252; protein YDL058w]
C:Species:	<i>Saccharomyces cerevisiae</i>
C:Date:	12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C:Accession:	S6793; A18455; S30782
R:Blocker, H.; Brandt, P.	
A:Submitted to the Protein Sequence Database, July 1996	
A:Reference number: S67587	
A:Molecule type: DNA	
A:Residues: 1-1790 <BLO>	
A:Cross-references: UNIPROT:Q07380; UNIPARC:UP1000052FC0; EMBL:Z74105; NID:91431058; PI	
A:Experimental source: strain S288C	
R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.	
J:Cell Biol. 113: 245-260. 1991	
A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp	
A:Reference number: A38455; MUID:91185402; PMID:2010462	
A:Accession: A38455	
A:Molecule type: DNA	
A:Residues: 1-389; 'A', 392-724; 'S', 726-1790 <NAK>	
A:Cross-references: UNIPARC:UPI00017B38P; EMBL:L03188	
A:Note: the authors translated the codon ACT for residue 768 as Ile	
R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.	
A:Submitted to the EMBL Data Library, February, 1993	
A:Description: An integrin analogue in <i>Saccharomyces cerevisiae</i> .	
A:Reference number: S30782	
A:Accession: S30782	
A:Molecule type: DNA	
A:Residues: 71-846; 'E', 848-923; 'K', 925-1252; 'I', 1254-1318; 'V', 1320-1460; 'S', 1462-1580; 'S	
C:Genetics:	
A:Gene: SGD:US01; INT1	
A:Cross-references: SGD:S0002216; MIPS:YDL058w	
A:Map position: 4L	
C:Keywords: coiled coil; transmembrane protein	
F:325-342/domain: transmembrane #status predicted <TM1>	
F:394-410/domain: transmembrane #status predicted <TM2>	
F:617-633/domain: transmembrane #status predicted <TM3>	
Query Match	
Best Local Similarity 5.8%; Score 318.5; DB 2; length 1790; Matches 217; Conservative 19.1%; Pred. No. 6.2e-06; Mismatches 392; Indels 307; Gaps 47;	
Db	977 KQILNNSHSLSKENFSLTEKLKVRSIDENTQLRQVLET-----KQNTA 826
Db	726 KLSFEVEKLQRCQTKLKQBITSL--OTETESTHENLTE----KULATNEHEKELDE 776
QY	103 AEKDLATINSNPFPDPDAALNPGDPSEBPETIASPRKEDSFHNSINPKVNP 162
Db	977 KQILNNSHSLSKENFSLTEKLKVRSIDENTQLRQVLET-----KQNTA 826
QY	163 --QYLNPNPDEPBEARTVIKSPPO--STPKRNTRPV-MSKYLTA-----DSSTKE 207
RESULT 8	
A46147	spectrin beta chain - fruit fly (<i>Drosophila melanogaster</i>)
C:Species:	<i>Drosophila melanogaster</i>
C:Date:	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession:	A46147; A33657
Db	923 -----BEMKIQCNLSE-----K 936
QY	328 HFRPDPLDYKSLNPQDITKENNKAYDGPASTGSRSLRPSDPMVLAIPDKLUTMVTYQ 387
Db	937 EHTSKELVYKS-----RFQSHDNLIVAKLTELKLSKLANNK 972
QY	388 -IRAHFGSGBLNVVOIEENSSKSTKVGVNTDTS-SVDQEKYAEUSDLKRP-E-LQ 444
Db	973 DMQAE--NESLIKAVEESKNESSKSIQNLNQKIDSMSQEQNFQINGSIENKIEQJK 1029
QY	445 PISGAVDFLUSQDPSVFVNDGVSERSESHOTPDHLSPTASPYCRRTKSDTBEPQKSCQS 504
Db	1030 TISBLEQ--TKEELIKSDSSKOBYESQISLAKKLEPAT-----TANDENVNKUSE- 1079
QY	505 SGRRSGSDPDPGCSNTSDTQAOLGKBRILKAT-TLSDLJUVSDKDKMSPPFICBT 563
Db	1080 -----LTKTREBLEALAAVKNLKNELTICKLETSEKALKEVENE-----EHL 1122
QY	564 DEQKLQTLDIGNSLEKEKLENSRL-ECRSDSPPIKTSLSPLSTSPLKAGYSYRSRDLA- 620
Db	1123 KRECIQ-----LEKATETKQQLNLSRQELKERAVALVLSQARDIAL 679
QY	621 -KKIGHASLRQTESDPADRTTLMHADHSKTVQHRLSROEELKERAVALVLSQARDIAL 679
Db	1161 LKKYQEIQANKERQYNEBISQNDIETTSIQGENESIKGGNDLSEGEVAKMSTSEBGSNL 1220
QY	680 KAGKHNNTATPFCNRQLSD--QDDEERRQRERARQOLLEARSGYKMSLSP-- SYG 734
Db	1221 K-----KSBTIAALNQIKEIACKKNETNEASILESTIKSVET--VKKIQLQEDCNPK 1270
QY	735 EMKAELKLERSKASGDENDN-IEID-TNBBEPGFGVVCGG-----DELTNL-----E 779
Db	1271 EKVYSELBDKUKASEDKNSKYLQLOKUSEKIKEBLDAKTEKIQLEKINTSKAKKSE 1330
QY	780 NDJ-----TPEBKSKVNLKKG-----LEVOPQVANSPSSPAQAVTES---- 821
Db	1331 SELSRLKKTSSEBRKNAEQLKLNQEIQKNAFEKERKELKLNQEGGSSTITQEVSEKINTL 1390
QY	822 -----SEQDMKGSTELRTERLQKTERFRNPVWVSKDSTVR 859
Db	1391 EDEBLIRLQNENELKAKIDNTSELEYVSLHDELLEBKONTIKSLODEILSYKDITRN 1450
QY	860 TQ-LQSFQSYIENPEMKQRSTQ1QDTKGNNTKAATETORKPSDSEBVLNKGKDTSQY 918
Db	1451 DEKLISTER--DMKRDLS--SKEQLRAQBSKAKWEGGLKLEERESSKERALESKE 1505
QY	919 VVGH-L-AMLENQKOIDRRAJAUVEKRYLMTGGRNTREEAMQEFMFLVNKKNALLR 977
Db	1506 MMKCKLESTIESNEELKSMETRKSDKLEOSKKSABEDINKNQ-----RHKSDLJSR 1559
QY	978 MNQSLSLRKEHDLRFLVLLNRLRMLA-----DWQTEAQKREBQILL--DLV 1028
Db	1560 IN-----ESEKQIE-----BLSKLURIRAKSGSLETVQELNNAQEKIRNAMENT 1606
QY	1029 ALYNKRDALVRLDQAQKAE-----EDE-----HLERTLEONKGKMKAKKEK 1072
Db	1607 VLKSKLIEDIERE-----KOKQAEKTSNQBKEKELTSRLKELEQOLDSTQOQAKSSEE 1660

A;Title: The complete sequence of Drosophila beta-spectrin reveals supra-motifs comprising the spectrin repeats	Proc. Natl. Acad. Sci. U.S.A. 89, 6187-6191, 1992	Author: R.A.; Winograd, E.; Due, J.; Brandin, B.; Branton, D.
A;Reference number: A46147; MUID:92335263; PMID:1631106		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-2291 <BYE>		
A;Cross-references: UNIPROT:Q00963; UNIPARC:UPI0000168B0B; GB:M92288; NID:9157019; PIDN:826; Note: sequence extracted from NCBI backbone (NCBIP:108607)		
R;Byer, T.J.; Hubain-Chisti, A.; Dubreuil, R.R.; Branton, D.; Goldstein, L.S.B.		
J. Cell Biol. 109, 1633-1641, 1989		
A;Title: Sequence similarity of the amino-terminal domain of Drosophila beta spectrin to A;Reference number: A33657; MUID:9009037; PMID:2677025		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-800 <BYE>		
A;Cross-references: UNIPARC:UPI000173DC2; GB:M92288		
C;Gene: FlyBase:beta-Spec		
A;Cross-references: FlyBase:FBgn003471		
C;Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleckstrin-like domain; actin binding; cytoskeleton		
C;Keywords: actin binding; cytoskeleton		
F;49-267-/Domain: alpha-actinin actin-binding domain homology <ACT>		
F;297-408-/Domain: Spectrin/dystrophin repeat homology <SPD>		
F;417-522-/Domain: Spectrin/dystrophin repeat homology <SPD>		
F;1698-1804-/Domain: Spectrin/dystrophin repeat homology <SPD>		
F;2146-2257-/Domain: Pleckstrin repeat homology <PLK>		
Query Match 5.8%; Score 316.5; DB 1; Length 2291; Best Local Similarity 20.0%; Pred. No. 1e-05; Mismatches 206; Conservative 169; MisMatches 295; Indels 359; Gaps 48; Matches 289		
Db 289 NASOSSLVWCKEVTKYKRGKITYFTTSRNGLSCFALLHFRPDLIDYKSLNPQDQN 349		
Db 170 SAKDALLWQCQMKTAGYHWNVRNFTTSRNGLAFALMAIKHRDLDVQPERKLSTNAHN 229		
Qy 349 NKKGAYD-GFASIGISRLSPLSDMVIALIDPLKLTWMTYQIRAHFS-----GQBL-N 398		
Db 230 LNNAFDVAEDKUGLAKLIDAE-VFVEHPDEKSITIYVVTYHYFSKLQBTVOGRICK 288		
Qy 399 VVIBENNSKTYKGVNFTD-----TNSVQDQBF-----YABLSLDR 438		
Db 289 VVGIAMENTKMDVYENFTSDLKKIETTQISGEREENSLAGVQGLAQPSVNTIEK 348		
Qy 439 EPLOQOPTISGAQVPLSODDSVFNDSVGCGESSESHQTP-DDHLSPTASPYCRTKSTIE 497		
Db 349 PPKEVE-KGNLEIL-----LFTIQSKORANNQKPYTPKGKOMISSDINGAWERKEKAE 401		
Qy 498 -----POKSOQSGRTS-----GSDPPG----- 515		
Db 402 RELARLEELRIOKEKLEQKARFDRKASHRMETWLSENORLVSQDNFGFDAAVEAAKHE 461		
Qy 516 -----ICSNIDSTQ-----AQVLGKRLKART-----LE 541		
Db 462 AIEFDIAYERYVQAVAVCDELESERYDVKRLLRNQMLWYLLBARRMIE 521		
Qy 542 LS-----DIXVSDKCKMSPPFPICBETDQKQLOTLIGSNT----- 577		
Db 522 ISLQLQQNQEMYLIDNNMEI-----KQLMTDYQKHLMGFDLQKHSVLEA 571		
Qy 578 -----EKEK---LENSRSLECRSPDES-PI-KTSLSPSKLGYSYSDLDLAKKHA 626		
Db 572 DINLGEBRVKVVQNSQKF-LSDPPESYKPCDPBPITIVSRVQOLBDAYALVLAVERRSR 630		
Qy 627 LQTSBSPDADRTLNHDHSKIVQHRLJSRQB--LKERARVILLEQARDIAKAGNK 684		
Db 631 L-----EBSRKLUWPFYDTEBENWIKERKEQV-----STDENG----- 664		
Qy 685 HNTTATPPCNROLSDQDEBERHOLRERAROLJATEAMSGVKUNSELPSYGMARKLKER 744		
Qy 665 HDLITV---NLMSKHKALE--SRTTSDFQLOQNAVKG--SELITEGHFGADRIKD 715		
Qy 745 SK-----ASCENDNEBIDT----NBRIPRGFVV 769		
Db 716 LKELINKWDHLDLDTKRRRELENAYEVQFLPADDDVWWMDLPRIVSSEDV----- 769		
Qy 770 GGGDELNLNEDLDPBONSKLVDLKLULEV---OPQVANSSAACKAVTSESQD 825		
Db 770 -GRDB-ANVSSL---KRDVDADELKNYABVIDALKHOAKSLSKLINEAKVND----- 818		
Qy 826 MKSGTEDLRLTERLQKTTERRNPVVFSKDSTVRKQ-LOSSQYIENRPEMKRQSQED 884		
Db 819 -----KRLAIDNRKVKELETAK--LRKGRLDALSLY---KMSRBDGVEQ 861		
Qy 885 TKGGNEKAAT-TETOKPSD-EVANGKFQDKTSQYVNGELAALENBOKQIDTRALVEK 943		
Db 862 IKB--KTKMLDLMTCQKJDBDVEIMKHFBS-----GFDKEMWANASRAVWNQ 908		
Qy 944 IRYLM-----DTGRUTERBAMMOWEMFLVNUKKALI----- 975		
Db 909 ARQLAVERHPSDETLBRONHNBWSTLKREKAEMDOLLSANGVOTFYBCRETMISI 968		
Qy 976 ---RMMQSLIYE---HDJLERRYELINREJRALMA-----IEDWQTEAQ 1016		
Db 969 EDKSRILTEPDTSLENDLTDQGWTQRLSGMDRDLAIQAKSSLREANSIDEHPEAK 1028		
Qy 1017 KRB---QULLOBELVALVNKRD-----LVRODQAQKOAERBDHEBERTLEQ 1061		
Db 1029 IIRERIAQTBLLIWQDQMLKERDSKLEERGDLRFLD-----HFQTLWK 1077		
Qy 1062 NKGNKAKKE 1070		
Db 1078 TOTDVAED 1086		
RESULT 9		
T4293 Probable spectrin beta chain - <i>Caenorhabditis elegans</i>		
C;Species: <i>Caenorhabditis elegans</i>		
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004		
C;Accession: T4293		
R;Austin, J.; Pratiss, V.; McKeown, C.		
Submitted to the EMBL Data Library, March 1998		
A;Description: Sma-1 encodes a SH-spectrin homolog required for <i>C. elegans</i> morphogenesis		
A;Reference number: Z22279		
A;Accession: T4293		
A;Status: preliminary; translated from GB/EMBL/DDBJ		
A;Molecule type: mRNA		
A;Residues: 1-463 <AU5>		
A;Cross-references: UNIPROT:Q02425; UNIPARC:UPI0000101013; EMBL:AF053496; PIDN:AAC08577		
C;genetics: smal		
Qy 402 RELARLEELRIOKEKLEQKARFDRKASHRMETWLSENORLVSQDNFGFDAAVEAAKHE 461		
Query Match 5.8%; Score 316.5; DB 2; Length 4063; Best Local Similarity 20.3%; Pred. No. 2.1e-05; Mismatches 204; Conservative 150; MisMatches 353; Indels 297; Gaps 41; Matches 206		
Db 516 -----ICSNIDSTQ-----AQVLGKRLKART-----LE 541		
Qy 542 LS-----DIXVSDKCKMSPPFPICBETDQKQLOTLIGSNT----- 577		
Db 542 LS-----DIXVSDKCKMSPPFPICBETDQKQLOTLIGSNT----- 577		
Qy 578 -----EKEK---LENSRSLECRSPDES-PI-KTSLSPSKLGYSYSDLDLAKKHA 626		
Db 572 DINLGEBRVKVVQNSQKF-LSDPPESYKPCDPBPITIVSRVQOLBDAYALVLAVERRSR 630		
Qy 627 LQTSBSPDADRTLNHDHSKIVQHRLJSRQB--LKERARVILLEQARDIAKAGNK 684		
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Qy 685 HNTTATPPCNROLSDQDEBERHOLRERAROLJATEAMSGVKUNSELPSYGMARKLKER 744		
Qy 665 HDLITV---NLMSKHKALE--SRTTSDFQLOQNAVKG--SELITEGHFGADRIKD 715		
Qy 745 SK-----ASCENDNEBIDT----NBRIPRGFVV 769		
Db 716 LKELINKWDHLDLDTKRRRELENAYEVQFLPADDDVWWMDLPRIVSSEDV----- 769		
Qy 770 GGGDELNLNEDLDPBONSKLVDLKLULEV---OPQVANSSAACKAVTSESQD 825		
Db 770 -GRDB-ANVSSL---KRDVDADELKNYABVIDALKHOAKSLSKLINEAKVND----- 818		
Qy 826 MKSGTEDLRLTERLQKTTERRNPVVFSKDSTVRKQ-LOSSQYIENRPEMKRQSQED 884		
Db 819 -----KRLAIDNRKVKELETAK--LRKGRLDALSLY---KMSRBDGVEQ 861		
Qy 885 TKGGNEKAAT-TETOKPSD-EVANGKFQDKTSQYVNGELAALENBOKQIDTRALVEK 943		
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Qy 944 IRYLM-----DTGRUTERBAMMOWEMFLVNUKKALI----- 975		
Db 909 ARQLAVERHPSDETLBRONHNBWSTLKREKAEMDOLLSANGVOTFYBCRETMISI 968		
Qy 976 ---RMMQSLIYE---HDJLERRYELINREJRALMA-----IEDWQTEAQ 1016		
Db 969 EDKSRILTEPDTSLENDLTDQGWTQRLSGMDRDLAIQAKSSLREANSIDEHPEAK 1028		
Qy 1017 KRB---QULLOBELVALVNKRD-----LVRODQAQKOAERBDHEBERTLEQ 1061		
Db 1029 IIRERIAQTBLLIWQDQMLKERDSKLEERGDLRFLD-----HFQTLWK 1077		
Qy 1062 NKGNKAKKE 1070		
Db 1078 TOTDVAED 1086		

R;Speicher, D.W.; Marchesi, V.T.
Nature 311, 177-180, 1984
A;Title: Erythrocyte spectrin is comprised of many homologous triple helical segments.
A;Reference number: A93341; MUID:84295638; PMID:6472478
A;Accession: B27016
A;Molecule type: protein
A;Residues: 292-324, 'X', 326-329, 'Y', 331-332;434-532;718-734, 'V', 736-773, 'X', 775-777;1031-1987 <SP>
A;Cross-references: UNIPARC:UPI0000173DBB; UNIPARC:UPI0000173DBC; UNIPARC:UPI000173BD
A;Note: the purified protein had a blocked amino end
C;Comment: Spectrin is a major structural component of the erythrocyte membrane cytoske
C;Genetics:
A;Gene: GDB:SPTB
A;Cross-references: GDB:119602; OMIM:182870
A;Map position: 14q23-14q23
C;Superfamily: spectrin beta chain; alpha-actinin actin-binding domain homology; spectr
C;Keywords: actin binding; cytoskeleton; duplication; erythrocyte; heterodimer; membran
F;53-271/Domain: alpha-actinin actin-binding domain homology <ACT>
F;53-112/Domain: spectrin/dystrophin repeat homology <SP01>
F;421-526/Domain: spectrin/dystrophin repeat homology <SP02>
F;527-635/Domain: spectrin/dystrophin repeat homology <SP03>
F;636-741/Domain: spectrin/dystrophin repeat homology <SP04>
F;742-846/Domain: spectrin/dystrophin repeat homology <SP05>
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F;953-1059/Domain: spectrin/dystrophin repeat homology <SP07>
F;1060-1166/Domain: spectrin/dystrophin repeat homology <SP08>
F;1167-1272/Domain: spectrin/dystrophin repeat homology #titin atypical <SP09>
F;1273-1377/Domain: spectrin/dystrophin repeat homology <SP10>
F;1378-1476/Domain: spectrin/dystrophin repeat homology <SP11>
F;1477-1582/Domain: spectrin/dystrophin repeat homology <SP12>
F;1583-1688/Domain: spectrin/dystrophin repeat homology <SP13>
F;1689-1795/Domain: spectrin/dystrophin repeat homology <SP14>
F;1796-1911/Domain: spectrin/dystrophin repeat homology <SP15>
F;1902-2007/Domain: spectrin/dystrophin repeat homology <SP16>
F;2008-2118/Domain: spectrin/dystrophin repeat homology <SP17>

Db 599 GYQPCDPQVIQDORMSHLQLCOPFEELSNMAAGARTOL-EGSKRLNKFPEWDEAESWIKEE 657
 Qy 730 LPSGEMALEK-----LKRSKASGDENDNIRDNTWEIP--GFVUGGIBLTLNEN 780
 Db 658 -Q1VSSLQDGKDLSVLTQKRGKAPEDLIGRHLQIFQBHQGMVA-----RN 707
 Qy 781 DLDTP--EONS KLVLDLKLUKLEQVOPQVANSPPSSAAQKVTESSRQDMKGSTDRLTRERL 838
 Db 708 EFGHQPIEARIKIKEYSAQMDQKLQDAFLCKGNLQDAENFQPQGDADDIKAWLQD---- 761
 Qy 839 QTTERFRNPVVSQDSTWRKTQLOFSOYIENRPEMKQRSTOBTDKKGNSBKAETT 898
 Db 762 --AHLISGBDVQDGEATRALKKKHDFPLE---ELBSRGWMEHLEO-----QA 806
 Qy 899 QRKPSDEVLNKGKFTDSYVUGLAALENEQKIDTRALVERGRYLMIDGRANTEER 958
 Db 807 QGPPEE-----FRD-SPDVTHRLQAKBLYQQVDAKDRDORLQMLDLYTFVGSTD 858
 Qy 959 AMQEWFMVLVKQNALIRMNQISLLEKEHDLLERYELNRELRAMLAED----- 1009
 Qy 859 A-CELM--MGEKEKWLAEEMPPTBLDEYVQHRFDLQDQMLTMQIDGVNLANSI 914
 Db 1010 -----WQ--KTEAQKRREQL-----LADP- 1026
 Qy 915 VESCHPRSRREVQYQDHATRWFQTLVSEERRAVDSLARVHTLCVDCERISKWIDKT 974
 Qy 1027 -----LVALVNKRDALVRD-----LQEQKQEE-EDEBLERLTLEONK 1063
 Db 975 KVVESTKDRGRDLAGITAQRKQUSGLERIVAVATQARVDALESRSQQLMDSPQ--KENTI 1032
 Qy 1064 GKMAKKEEK 1072
 Db 1033 GQRQXHLES 1041

RESULT 12

T29140 hypothetical protein K1C4.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T29140
 R;Pauley, A.;Gartung, S.
 A;Submitted to the EMBL Data Library, July 1996
 A;Description: The sequence of *C. elegans* cosmid K1C4.
 A;Reference number: Z20577
 A;Accession: T29140
 A;Status: preliminary, translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2326 <PAU>
 A;Cross-references: UNIPARC:UPI00003588F; EMBL:U64954; PIDN:AAB18316.1; GSPDB:GN00023;
 A;Experimental source: strain Bristol N2; clone K1C4
 A;Gene: CESP:K1C4.3
 A;Map position: 5
 A;Intcons: 105/1; 131/3; 155/3; 449/3; 2075/1; 2140/3; 2182/1; 2232/2; 2309/1
 C;Superfamily: spectrin beta-G chain; alpha-actinin actin-binding domain homology; pleck

Query Match 5.6%; Score 309; DB 2; Length 2326;
 Best Local Similarity 20.1%; Pred. No. 2.2e-05;
 Matches 201; Conservative 174; Mismatches 327; Indels 300; Gaps 44;

Db 289 NIASQSLLYWCKEVTKNYTRGVKLTINFTTSWRNGLISFCATLHHFRPDLIDYKSLNPQDTKEN 348
 Qy 229 SAKKEALLWCMQKMTAGYFVNWNKFSTSWRDGLAFNALIHKRPDLWDYDNOKSALYN 288
 Qy 349 NKGYADGFS-TCISRLIEPSPDMYLAPDKLWTMYQIRAHFS-----GOILANV 399
 Db 289 LOSAFDTAENQIGLAKFLDAE-VNVQDPEKSIITVYVYFNKLUQDINTQGRIGK 347
 Qy 400 V--QIRENSKSKTYKVGVYBTDMNSVD-----QKFFAELSDLKRPBLOQPO 447
 Db 348 VNELMENDK--MINRYETLSSDLWWINAKIQMLNERHFENNLSCGVQD-----LT 397

RESULT 13

T8296 myosin heavy chain - *Entamoeba histolytica*
 C;Species: *Entamoeba histolytica*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T18296
 R;Guillen, N.
 A;Reference number: Z18865
 A;Accession: T18296
 A;Status: preliminary, translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2139 <GU>
 A;Cross-references: UNIPROT:Q07569; UNIPARC:UPI00000802D3; EMBL:L03534; NID:91850912; PII
 C;Genetics:

C;Gene: mhcA	F;91-780/Domain: myosin heavy chain; myosin motor domain homology <M0>
Query Match	5.4%; Score 299; DB 2; Length 2139;
Best Local Similarity	20.2%; Pred. No. 5.2e-05;
Matches	254; Conservative 213; Mismatches 448; Index 340; Gaps 53;
QY	38 PLRREGKATBDMOSL-----ASLYSMQADIGNLDDFERDNEEDDENRVNQ 83
Db	859 FEERGKKKDKKEIEDLKKKLAEEIKKREAAENALASATAKTEAKIQLED----- 910
QY	84 ERKAKITILINKINP----IDEAKDLATWSNPDPDAEL----NPPGD----- 128
Db	911 -----KISELESKAELDKOELNLTKTENL---EDEKBEKLETIDNLKGDLKDSKLKG 961
QY	129 PDSRBRPIETASPRTEFSYNNSNPFFEVQTPQQLNPDEPFAFV----- 177
Db	962 EDLVEIEFLNSQINTLNATVDKDKTIAEMQ----ESIDEKEDEBTIKLGDIKLLRR 1016
QY	178 KDSPPPOSTKRKNTRPPVDMSKYL-----DSKTEBERLDNSPPYRKSTPPN 227
Db	1017 KDDLEQDRADVSATKDDIAKLNKNTICEDAKDDETAKUQELEDEN-----KNN 1067
QY	228 NLVNPWQEL----ETERRVKRKAAPPULSPKTFGVNLVENTISAGKDLTSKPSSPIPSP 282
Db	1068 DLTTNEQDQTOLQKGETEKSLSLAQWATKKAASDERTDTLSQN----- 1107
QY	283 VLGRKPNASQLLWCKETVNTRGKVITNFPTSWWRNGLSFCALMHIFRPDLTDYKSIMP 342
Db	1108 -LENKLTQKLNLTWKADLEKKSGIK----- 1139
QY	343 QDIEKENNKAYDGFPASIGISRLRPLPSDMVTLALPDQLT----VMTYQYQIRAHPSG 395
Db	1140 ---EDDKNKGED-----LRAAQKIKELDDEITKAGDVQSYLQKQKBEYESQIAK 1187
QY	396 --ELNVQIERSSKSTKVGVYEDT-NSSYDQKBYTAELSDLKRPBLQPOPIGAVD 451
Db	1188 MOREKEATGNDVKKNKEKTIKEKELEIQLQEKUDETEVTEKEDE-KKKKEIKEKEMAL-- 1244
QY	452 FLSQDDSVFVNDJSGVGEBSESEHOPDDHILSPS-----TASPYCRRTKS-DTEPKSQSQ 503
Db	1245 --QEKEKV-ESSKNISETDKKKLEDNLKDOKKDDMTADNEKKAKAKAKDQALEV 1300
QY	504 SSVRTSGSDPGCISNTSTOAQYTLGKQRLLKARTELSDLVSDKDKMSPPRCRET 563
Db	1301 QDNHEKAVADAEELINKKKQASDKELNLSKAEELAKTAKSVVUESKNDKSENKAASBEI 1360
QY	564 DEQKLQTLDIGSLKKEKLENSLSLCBDSPEPIKK--TSLSPTSKIGKYSRSRDL-- 618
Db	1361 DQANEKLNQIADLRKATADLQEQANKEVQAQRDKVADNKOMTKLEETKARDENT 1420
QY	619 -----LAKKQHSLRQTESPDDADRTLNHADHSKIVORHLRSRQEELK--ERA 666
Db	1421 YKVENYEVKURKEADLSEANELDIEKKDRMKVKOVKKLGSEELKETDKUNAAAEKD 1480
QY	667 RVLLEQARDAALKAGKNC----HNTNTATPPCNROLS----DQDDEERRRERA-- 714
Db	1481 SIFTAKKOSDADLRELNKTVBEEHDBBVAK-LNTQITKLTDRNQSBRELNLRSKADKD 1538
QY	715 RQIJAARSGVMSLPSYGYMAEK-----LKERSKASSGDENDNIDTNE- 761
Db	1539 KKKISLEBEQWNELESRPGTGANWADNEKIRDAQIADLNKALEMKVQNNLQLQATKEL 1598
QY	762 -----EIPGEFGVGGDDELTMELNDLDTPEBONS----- 796
Db	1599 KAKONDILTSKIEITE-----NEMKKLENAKKGLLEQDKDEADKAWBQTIKRGKIGKEEV 1651
QY	797 KKL-LKVPQ----QVANSPSSAAKAVTTESSQDMKSCHEDELTTERL-----QKUTTER 844
Db	1652 KKLUTETIOALKFOI-NAPSSVAQEEBKORLESIDIAELKQBOLEQRTTANAAERKKIQA 1710
845 FRNPVVFES-KDSTVRKTOLQSSQYIERNRPMKRQRSIQBDTQKGNIEKAATETQRKPS	903
RESULT 14	
528916	dystrophin - mouse
N;Alternate names:	duchenne muscular dystrophy protein
C;Species:	Mus musculus (house mouse)
C;Date:	22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession:	S29916; S27162; S10922; C43837; B4134
R;Bies, R.D.; Phillips, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.	Nucleic Acids Res. 20, 1757-1751, 1992
A;Title:	Human and murine dystrophin mRNA transcripts are differentially expressed during development.
A;Reference number:	S28916; MUID: 92853376; PMID: 1579466
A;Accession:	S29916
A;Status:	preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type:	mRNA
A;Residues:	1-3578 <1E>
A;Cross-references:	UNIPARC:UPI000027987; EMBL:M68859
A;Title:	Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary analysis.
A;Reference number:	A90897; MUID: 87273512; PMID: 3607877
A;Accession:	B27162
A;Status:	not compared with conceptual translation
A;Molecule type:	mRNA
A;Residues:	1-201 <KOB>
A;Cross-references:	UNIPARC:UPI0000177686
R;Nudel, U.; Zuk, D.; Einat, P.; Zeezon, B.; Levy, Z.; Neuman, S.; Yaffe, D.	Nature 337, 76-78, 1989
A;Title:	Duchenne muscular dystrophy gene product is not identical in muscle and brain.
A;Reference number:	S06461; MUID: 89082658; PMID: 2909892
A;Accession:	S10922
A;Status:	translation not shown
A;Molecule type:	mRNA
A;Residues:	1-106 <NUD>
A;Cross-references:	UNIPARC:UPI0000177687; EMBL:X14183
R;Rapport, D.; Lederle, D.; den Dunnen, J.T.; Grootenhuis, P.M.; Van Ommen, G.J.; Diffenbacher, A.; Resdries, M.; Marshik, 3059-3181 <RA>	Differentiation 49, 187-193, 1992
A;Title:	Characterization and cell type distribution of a novel, major transcript of the Duchenne muscular dystrophy gene in mice and humans.
A;Reference number:	A40134; MUID: 880018015; PMID: 3659917
A;Accession:	B4134
A;Status:	preliminary
A;Molecule type:	mRNA
A;Residues:	300-676, F, 678-1390 <HOF>

A: Cross-references: UNIPARC:UPI0000177589; GB:M18025 C: Genetics: A: Introns: 11/1 C: Superfamily: dytrophin, alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology <SP1> F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT> F:340-449/Domain: spectrin/dystrophin repeat homology <SP2> F:279-294/Domain: spectrin/dystrophin repeat homology <SP3> P:304-B-3085/Domain: WW repeat homology <WW1>	Db 724 KRLD--VDTLEHWSWITRSEAV---LQSFEPFAVKGKNTISDL---QEVKNAIREKAE 774 QY 943 RLRYLMDGRNTS-----EEAMMQEWPMFLVNNKALIRRMMQ-LSLKEKHD 990 Db 775 KERKLQDSRSQADLVEQMANEGUNASIROSEQUISWTFQQLISERVWUYEYQNI 834 QY 991 ERREVLLNRELMLATEDDWQKTE-----AOKRREBOLLIDELVALVNRKDAL--VR 1039 Db 835 ITFYNQOLQOLQMTTAAEULKIQSTWUSETPEAIKSQQLICKDE---VNRULSALQFQIE 890 QY 1040 DLQAQEKQAEEDBE 1053 Db 891 QLKIQSULQKKEKQ 904
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